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Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                    Result
                                                                                                                                                                                                                                                  ŏ.
                                                                                                                                                                                                                                                                                                                                                pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
648
552
544
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523.5
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                                                                                                                                                                                                                                                  Score
                                                                                                                                                                655
655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             May 7, 2002, 12:22:25; Search time 67.39 Seconds (without alignments) 135.198 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-155-739-11
                                                                                                                                                                                                                                                                           Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1988.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1988.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*

/SIDSB/gcgdata/geneseq/geneseqp/AA1991.DAT:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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  123
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                                                                                                      AAR81323
AAR81333
AAW22428
AAW22413
AAR81330
AAR81327
                      AAB30693
AAR76681
                                                                AAW22410
AAW44124
                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                  Humanized VLA-4 an
Human VLA-4 reshap
Humanised alpha-4
Humanised alpha-4
                                                                                                                                                                                                                                                           Description
      Chimaeric human/mu
                                            Heavy chain variab
A fusion of single
                                                                                         Alpha-4 integrin m
                                                                                                          Mouse anti-VLA-4 a Mouse VLA-4 antibo
                            Human/murine chime
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84.	484.5	486	486	487	487	487	487	487.5	489	489	489.5	491	491	492	492	492	493	493	495	496	499	499	503	0	504.5	507.5	512	512	515	515	523	523
74.0	74.0		74.2	74.4	74.4	74.4		74.4	74.7	74.7	74.7	ū		75.1	75.1	Ģ	ū	5	75.6	75.7	٥.	6	76.8	5	7			•		78.6		79.8
139	139	143	140	119	119	119	119	120	119	119	120	119	119	136	117	117	119	119	119	136	119	119	119	119	118	135	119	119	119	119	269	269
21	14	15	18	22	22	20	20	15	22	20	18	22	20	15	17	15	22	20	16	17	22	20	22	20	14	21	18	16	18	16	17	16
AAY56877	AAR33953	AAR59942	AAW21847	AAB74976	AAB74973	AAY52715	AAY52712	AAR47491	AAB74981	AAY52720	AAW27551	AAB74969	AAY52708	AAR57481	AAR92079	AAR57476	AAB74979	AAY52718	AAR81331	AAR92084	AAB74980	AAY52719	AAB74978	AAY52717	AAR37611	AAB07969	AAW22425	AAR81324	AAW22426	AAR81325	AAW04397	AAR76682
gH1 variable domai	CDR-grafted humani	Anti-VLA4 rad nulla	heav	ATK-5	ATK-0		ATX		ATK-5	AIX	neavy	D ATK-D	AIR	LUCOF	1005	ורפת שוורד	Humanised Aix on	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7				ALA C		-	ı	y chain var	manise		ardra	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	VI.A-A	-M21 ar

ALIGNMENTS

AAR81323 RESULT

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AAR81323 standard; Protein; 123 AA

AAR81323;

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Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
                                                                                                                                                                                                                                       Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                 02-APR-1996 (first entry)
                                                                                                                                                                  27-JUL-1995
                                                                                                                                                                                       WO9519790-A1
                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                               antibody engineering.
                                                                                                                          25-JAN-1994;
 Claim 11; Page 69; 105pp; English
                             New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                             WPI; 1995-269276/35.
                                                                                 Bendig MM, Jones TS,
                                                                                                                                               25-JAN-1995;
                                                                                                     (ATHE-) ATHENA NEUROSCIENCES INC.
                      inflammatory disease.
                                                                                                                           94US-0186269.
                                                                                                                                                 95WO-US01219
                                                                                   Leger OJ, Saldanha J;
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AAR81333
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Best Local :
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                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                               HOMO sapiens
                                                                                                                                                                                                                                                                                                                      Human VLA-4 reshaped antibody 21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                             Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                       antibody engineering.
                                                                                                                                                                                                                                                                                                                                                        23-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           AAR81333;
                                                                                                                                                                                                                                                                                                                                                                                                               AAR81333 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence encodes the mouse antibody 21.6 heavy chain variable region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AA099889 and AA099892) regions are linked to human constant regions in the construction of a humanized modified using pCR primers (See AA099895-98) and then subcloned into constant regions. In the humanized light chain, maino acids L45, L58 and L69 in the humanized light chain, anino acids L45, by the amino acid present in the equivalent position of the mouse blaced annotating dispersions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating inflammatory diseases such as multiple sclerosis can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-idiotype antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitis or encephalitis.
detecting VLA-4, for affini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 vss 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 AA;
                                                                                                                                    /note=
55..68
                                                                                                                                                               /note-
50..54
                         /note= "complementarity determining region 3"
132...142
                                                 /note= "framework region 3"
118..131
                                                                                          /note-
                                                                                                                /note= "framework region 2"
                                                                                                                                                                                                  /note= "signal peptide"
                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 655; DB 1 100.0%; Pred. No. 4e-53;
    "framework region 4"
                                                                                _"complementarity determining region
                                                                                                                                       "complementarity determining region
                                                                                                                                                                       "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB_16; Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW22428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis;
                                                                  Humanised alpha-4 integrin antibody 21.6 VL version Ha
                                                                                                          09-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse cDNAs are modified using PCR primers (AAQ)9895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized heavy chain, amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced by the amino acid present in the equivalent chimeric antibodies are transfected into COS cells. The humanized entibodies can be used to inhibit adhesion of a leukocyte to an sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can enacting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
                                                                                                                                                AAW22428;
                                                                                                                                                                           AAW22428 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents the human reshaped antibody 21.6 heavy chain variable region against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ99889) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                   140 vss 142
                                                                                                                                                                                                                                                                                                   121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 11; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ99894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bendig MM, Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                       61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                      20 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JUL-1995.
                                                                                                                                                                                                                                                                                                                                                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                       \tt dpkfqgrvtitadtsastaymelsslrsedtavyy caregyygnygvyamdywgqgtlvt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1995-269276/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0186269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 655; DB 16; 100.0%; Pred. No. 4.7e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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cc region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also cc AM22413). It is composed of complementarity determining regions from cc AM22413). It is composed of complementarity determining regions from cc the VH region (see AM22410) of mouse alpha-4 integrin monoclonal cc antibody 21.6 and a modified human 21/28'CL framework. It can be composed in mammalian host cells following PCR amplification and cc mutagenesis of appropriate mouse and human DNA sequences. The cc humanised 21.6 VH and a humanised 21.6 vL (see AAM22412) can be used to produce a claimed humanised 21.6 antibody that is useful in the cc manufacture of a medicament for treating asthma, atherosclerosis, dementia, diabetes, inflammatory bowel disease, rheumatoid cc arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial cc eschaemia, and acute leukocyte mediated lung injury. The humanised cantibody has a half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                    21-NOV-1995;
                                                                                                                                                                                                                                                                                                   Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT74789
                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                            Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                      (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-may-1997
                                                                                                                                                                                                                                                                                      asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                            Example 6; Fig 11; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO
                                                                                                                                                                                                                                                                                                                                                                            Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Mat_protein
/note= "VH version Ha (Claim 25)"
20..49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US18807.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR2
/note=_ "21.6 complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "21/28'CL framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR1
/note= "21.6 complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= FR3
/note= "21/28'CL framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "21/28'CL framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "21.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
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                                                                                                                                                                                                                                                                                                                                                                              Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                 Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                    Yednock TA;
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Вb
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Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW22413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised alpha-4 integrin antibody 21.6 VH Ha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW22413 standard; Protein; 123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                           /note= "21/28'CL framework region 1" Misc-difference 27..30
                                                                                                                                                                                                                                                                                                                                                                 Chimeric
                                                                                                                                                                                                                                                                                                                                                                            Chimeric
                                                                                                                                                                                                                                                                                                                                                                                      Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 vss 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 VSS 123
                                                                                                                                                                                                                                                    Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqriewmgridpangytky 79
                                                                                                                                                                                     Region
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                                                                                                                      Misc-difference
                                                                                                                                                     Region
WO9718838-A1
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                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                        /label= CDR3
/note= "21.6 complementarity determining region 3"
113...123
                                                                                                                                                                                                                                                                                       /note= "21/28'CL
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                /label= CDR1
/note= "21.6 complementarity determining region 1"
                                                                                                           /note= "21/28'CL
                                                                                                                                /note= "21/28'CL framework region 3"
                                                                                                                                            /label= FR3
                                                                                                                                                                 /label= CDR2
/note= "21.6 complementarity determining region
                                                                                                                                                                                                  'note= "21/28'CL framework region
                                                                                                                                                                                                              /label= FR2
                       /note= "21/28'CL framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 655; DB 18; 100.0%; Pred. No. 4.7e-53;
                                                                                                                                                                                                                                                                  binding"
                                                                                                                                                                                                                                                                             those of MAD
                                                                                         loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                 VL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                          residues 27-30 are replaced by
                                                                                                  important in supporting the CDR2
                                                                                                              Arg-72 is substd. by Ala of mouse
                                                                                                                                                                                                                                                                                21.6, involved in antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
            Mùs musculus
                                   antibody engineering.
                                        Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                        Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
                                                                                                                                                                      AAR81330 standard; Protein; 123 AA
                                                                                                            02-APR-1996 (first entry)
                                                                                                                                                AAR81330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     manufacture of a medicament for treating asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin generating idiotypic antibodies. The humanised antibody has a first in the human circulation essentially equivalent to that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This polypeptide, designated Ha, comprises the heavy chain variable region (VH) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human 21/28/CL framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used to produce a claimed humanised 21.6 antibody that is useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of naturally occurring human antibodies.
                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; Fig 7; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                61 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyandywgqgtlvt 120
                                                                                                                                                                                                                                                                                                              61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGYYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-297879/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                          1 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                        1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                      vss 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0561521
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                                                                                                                                                                                                                                                                                                                                                                                                                                             98.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 648; DB 18;
Pred. No. 1.8e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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CC The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain CC wariable region (without signal sequence). Cloned cDNA CDR sequences of comouse 21.6 variable light and variable heavy regions are linked to human CC constant framework regions of the REI antibody for the light chain and CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are CC modified using PCR primers (See AAQ9895-99) and then subcloned into CC constant regions. In the humanized light chain, amino acids L45, L49, CC L58 and L69 in the humanized light chain, amino acids L45, L49, CC constant regions. In the humanized light chain, amino acids L45, L49, CC constant regions. In the humanized light chain, amino acids L45, L49, CC clain. Plasmids encoding the chimeric antibodies are transfected into CC cells. The humanized antibodies can be used to inhibit adhesion of a CC leukocyte to an endothelial cell and to treat inflammatory diseases such CC cerebral traumas, meningitis or encephalitis. The antibodies can also be used in the treatment of stroke, CC cerebral traumas, meningitis or encephalitis. The antibodies can also be can did for detecting VLA-4, for affinity purification or for generating CC anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FT FT
Sequence
                                                                                                                                                                                                                                                                                                             Disclosure; Page 68; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                      New humanised antibodies against VLA-4 - used for inhibiting
                                                                                                                                                                                                                                                                                                                                                   inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-269276/35
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09519790-A1
                                                                                                                                                                                                                                                                                                                                                        leukocyte adhesion to endothelial cells, partic. for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "mouse heavy chain variable complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "mouse heavy chain variable framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "mouse heavy chain variable framework
    region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= FR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "mouse heavy chain variable complementarity
determining region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "mouse heavy light chain variable framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "mouse heavy chain variable complementarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   determining region
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AAR81327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR81327;
                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse VLA-4 antibody 21.6 light heavy variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR81327 standard; Protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1996
                                                                                                                                                                                                                                                                                                                                                          Region
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                                                                                                                                                                                                                              WO9519790-A1
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                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                     25-JAN-1994;
                                                                                                                                                                                       25-JAN-1995;
                                                                                                                                                                                                          27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
The sequence represents the mouse antibody 21.6 heavy chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
                                                                  New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                     Disclosure; Fig 2; 105pp; English.
                                                                                               N-PSDB; AAQ99892
                                                                                                           WPI; 1995-269276/35.
                                                                                                                                                (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                            inflammatory disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGYYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                     94US-0186269
                                                                                                                                                                                         95WO-US01219.
                                                                                                                                                                                                                                                                                                                                         /note=
55..68
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50..54
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                    note= "complementarity determining region
                                                                                                                                                                                                                                                                                        /note-
                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.9%; Pred. No. 1.2e-43;
                                                                                                                                                                                                                                                                                 ..131
                                                                                                                                                                                                                                                                                         "framework region 3"
                                                                                                                                                                                                                                                                                                            "complementarity determining region
                                                                                                                                                                                                                                                                                                                              "framework region 2"
                                                                                                                                                                                                                                                                                                                                                  "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                      "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                         "signal peptide"
                                                                                                                               Leger OJ,
                                                                                                                                                                                                                                                   "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                  Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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                                                                          for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized heavy chain, amino acids H27, constant regions. In the humanized heavy chain, amino acids H27, constant regions. In the equivalent position of the mouse by the amino acid present in the equivalent position of the mouse Clif g H chain. Plasmids encoding the chimteric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for anti-inflammatory purification or for generating captividators.
                                                                                                                                                                                                                                                                AAW22410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                  asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW22410 standard; Protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW22410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-4 integrin mouse MAb 21.6 VH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-1997
                                                                                                                                                                                                                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 V 121
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                                                                                                                                                                                            Region
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                                                                                                                                                                                                                                                                                 Peptide
                                 Region
                                                                                    Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewlgridpangytky 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                /note= "framework region 1"
50..54
                                                                                                                                                                                                                                                                    /label= Leader
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                /label= FR1
/note= "framework region 3"
                                                                                                                                                              /note
                                                                                                                                                                               /label=
                                                    /label- CDR2
/note- "complementarity determining region
                                                                                                         /note= "framework region 2"
                    /label= FR3
                                                                                                                            'label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.1%;
82.6%;
                                                                                                                                                            "complementarity determining region 1"
                                                                                                                                                                                 CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 544; DB 16; Length 140; pred. No. 7.5e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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complementarity determining regions (CDRs) of the 21.6 VH can be incorporated into a human 21.78 CL framework to produce a claimed in humanised 21.6 VH can be charmed 21.6 VH (see AAW22413) and a claimed humanised 21.6 VH can be cantibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, carthritis, transplant rejection, graft versus host disease, tumour metastasis, naphritis, atopic dermatitis, provided the season of the constant of the manufacture metastasis, and acute leukcoyte mediated lung injury. The antibody for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibodies of the convenion have a half-life in the human circulation essentially
            Heavy chain variable region of humanised NR-LU-13 antibody NRX451
                                                      05-JUN-1998 .(first entry)
                                                                                                AAW44124;
                                                                                                                       AAW44124 standard; Protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                  140 v 140
                                                                                                                                                                                                                                                    121 V 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polypeptide comprises the heavy chain variable region (VH) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 69-70; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bendig MM,
                                                                                                                                                                                                                                                                   80 dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvyamdywgqgtsvt 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9718838-A1
                                                                                                                                                                                                                                                                                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGYYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                    20 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 79
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                                                                                                                                                                                                                                                                                                                                                             100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95us-0561521.
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/note= "complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                             83.1%; Score 544; DB 18; 82.6%; Pred. No. 7.5e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leger OJ, Saldanha J,
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                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 140;
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                                                                                          AAB30693
                                                                                                            RESULT
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Best Local :
02-APR-2001 (first entry)
                                                                 AAB30693 standard; Protein; 431 AA.
                                       AAB30693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. The hAb, specifically NRX451, or its conjugates can be used for the manufacture of a diagnostic or medicament for cancer diagnosis or treatment. The hAb has reduced immunogenicity and toxicity in
                                                                                                                                                           118 vss
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        humans, but retains the ability to bind the NR-LU-13 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            humanised murine anti-human cancer antigen antibody (Ab)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the heavy chain variable region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 4; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised antibody binds same human cancer antigen as antibody NR-LU-13 - useful for pre-targeting methods, conventional antibody therapy and immunodiagnosis
                                                                                                                                                                                              121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-042124/04.
                                                                                                                                                                                                                                               61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1996;
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antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment.
                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                               1\ \mathsf{qvqlvqsgaevkkpgasvkvsckasgfnikdtymhwvrqapgqglqwmgridpangntkc}
                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHMVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                         9
                                                                                                                                                                                                              dlsfqgrvtitadtsintaymelsslrsddtavyycsrevl---tgtwsldywgqgtlvt 117
                                                                                                                                                                                                                                                                                                                                                                 102;
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 AA;
                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0660362
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                                                                                                                                                                                                                                                                                                                                                                            79.9%;
82.9%;
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                                                                                                                                                                                                                                    Hylarides MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                                                                                                                                                                                                                                        Score 523.5; DB Pred. No. 4.9e-41
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mallet RW,
                                                                                                                                                                                                                                                                                                                                                                                         DB 19; Length 120;
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The present sequence encodes a fusion of the single chain antibody CC hNNR-IU-10 and streptavidin. The antibody binds the antigen ECP40 or CC EPCAM. The fusion protein is expressed using vectors of the invention. CC The specification describes vector constructs for expressing streptavidin CC fusion proteins. The vector comprises a first nucleic acid encoding CC streptavidin or its functional variant operatively linked to a promoter, CC and a cloning site for insertion of a second nucleic acid sequence CC encoding a polypeptide to be fused with streptavidin, interposed between CC the promoter and the first nucleic acid sequence. Alternatively, the CC vector construct comprises a first nucleic acid, operatively linked to a CC promoter, encoding a polypeptide to be fused with streptavidin, and a CC cloning site for insertion of a second nucleic acid, encoding at least CC 129 amino acids of streptavidin or its functional variant. The fusion CC associated with cancer, e.g. adenocarcinomas or hematological CC associated with cancer, e.g. adenocarcinomas or hematological CC mallgnancies. The vector construct is useful for expressing of CC for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian CC host
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A fusion of single chain antibody/streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated cancer, e.g. adenocarcinomas – \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1999;
03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-2000; 2000WO-US15595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 10; 100pp; English.
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                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                148
                               121
 265 vss 267
                                                                                                 61
                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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DB; AAC86562.
                                 VSS 123
                                                              DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                           qvqlvqsgaevkkpgasvkvsckasgfnikdtymhwvrqapgqglqwmgridpangntks 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sc,
                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                 431
                                                                                                                                                                                                 Conservative
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99US-0168976.
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                                                                                                                                                                                                                79.9%;
82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schultz JE,
                                                                                                                                                                                                 8
                                                                                                                                                                                                                Score 523.5; DB Pred. No. 2e-40;
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin Y,
                                                                                                                                                                                                                                DB 22;
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                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                Length 431;
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AAR76681
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                                                                                 Query Match
Best Local S
Matches 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               medulloblastoma; brain tumour; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; murine; chimeric antibody; HEF-RVL-M21g(gamma)1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human/murine chimeric antibody HEF-RVL-M21g(gamma)1.
                                                                                                                                                   AAQ94539 encodes AAR76681 the human/murine chimeric antibody HEF-RVL-M21g(gamma)1. The antibody is reactive with human medullo-blastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this disease.
                                                                                                                                                                                                                                    Reconstituted antibody against human medullo:blastoma cells contains high proportion of human antibody origin and has low
                                                                                                                                                                                                                                                                                                 Ohtomo T, Sato K,
                                                                                                                                                                                                                                                                                                                                          19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                             19-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                     WO9514041-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                 Sequence
                                                                                                                                                                                                       Claim 26; Page 94; 120pp; Japanese.
                                                                                                                                                                                                                           antigenicity
                                                                                                                                                                                                                                                                    N-PSDB; AAQ94539.
                                                                                                                                                                                                                                                                              WPI; 1995-200347/26.
                                                                                                                                                                                                                                                                                                                    (CHUS ) CHUGAI SEIYAKU KK.
    80
            20
                                                   QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 133
                                        qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 79
                                                                                   103;
                                                                                            Similarity
                                                                                                                                    136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                          93JP-0291078
                                                                                                                                                                                                                                                                                                                                                              94WO-JP01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CDR 1
56..59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= FR 1
51..55
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= FR 3
119..126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR 2
87..118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= sig_peptide 20..50
                                                                                                                                                                                                                                                                                                                                                                                                                        /label- FR 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= FR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= CDR 3
                                                                                                                                                                                                                                                                                                 Tsuchiya
                                                                                           79.8%;
83.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    136
                                                                                   4; Mismatches
                                                                                            Score 523; DB 16;
Pred. No. 6.2e-41;
                                                                                                                                                                                                                                                                                                  ×
                                                                                     10;
                                                                                                      Length 136;
                                                                                     6;
                                                                                    Gaps
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Š

123

δõ

Matches

103;

Conservative

4;

Pred. No. 6.2e-41; 4; Mismatches 10; Mismatches

Indels

6

Gaps

2

83.7%;

Best Local Similarity

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The present sequence is a fragment of the chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols. was prepd., and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain DNA mols. sepd. and connected with a peptide linker to produce a single stranded Fv region. The reshaped Fv region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW04396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
Sequence
                          e.g. myeloblastoma.
                                                                                                                                                                                                                                   Example 5; Pages 38-39; 45pp; Japanese.
                                                                                                                                                                                                                                                                       Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and
                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT38653.
                                                                                                                                                                                                                                                                                                                                                                                            18-OCT-1994;
19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-1996.
                                                                                                                                                                                                                                                             treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP08169900-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity;
                                                                                                                                                                                                                                                                                                                                                                (CHUS ) CHUGAI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21-g(gamma)1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis; treatment; cerebral tumour; reshaped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW04396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW04396 standard; Protein; 136 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 vss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                     1996-358509/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136
136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         94JP-0252166.
93JP-0291078.
                                                                                                                                                                                                                                                                                                                                                                                                                                 94JP-0285057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= CDR_2
118..125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= CDR_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= sig_peptide
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Query Match

79.8%;

Score 523;

DB 17;

Length 136;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR76682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                        AAQ94548 is the plasmid pSCFVT7-hM21, which encodes AAR76682 the human antibody ONS-M21 FV fragment. The plasmid was used in the construction of an expression vector, contg. cDNA encoding a human/murine chimeric antibody, reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be
Sequence
                  used in the diagnosis and treatment of this disease
                                                                                                                          Reconstituted antibody against human medullo:blastoma contains high proportion of human antibody origin and
                                                                                          Claim 35; Pages 98-99; 120pp; Japanese.
                                                                                                                   antigenicity
                                                                                                                                                                                                                                     19-NOV-1993;
                                                                                                                                                                                                                                                                               26-MAY-1995.
                                                                                                                                                              N-PSDB;
                                                                                                                                                                                             Ohtomo T,
                                                                                                                                                                                                                 (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                         19-OCT-1994;
                                                                                                                                                                                                                                                                                                     W09514041-A1
                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pSCFVT7-hM21; human; ONS-M21 antibody; chimeric medulloblastoma; brain tumour; treatment; diagnosis; Fv
                                                                                                                                                                                                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ONS-M21 antibody Fv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR76682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR76682 standard; Protein; 269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 vss 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 133
                                                                                                                                                                       1995-200347/26.
                                                                                                                                                             AAQ94548
                                                                                                                                                                                           Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                     93JP-0291078
                                                                                                                                                                                                                                                          94WO-JP01763.
                                                                                                                                                                                                                                                                                                                                                                           /note= "
140..154
                                                                                                                                                                                                                                                                                                                       /note= "FLAG"
                                                                                                                                                                                                                                                                                                                                  262..269
                                                                                                                                                                                                                                                                                                                                                        155..269
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       note= "light variable region"
                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                       /label= sig_peptide
                                                                                                                                                                                           Tsuchiya M;
                                                                                                                                                                                                                                                                                                                                                                "linker"
                                                                                                                                                                                                                                                                                                                                                                                   "heavy variable region"
                                                                                                                           cells -
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fragment.
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Length 269;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity; diagnosis; treatment; cerebral tumour; reshaped.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimaeric human/murine MAb ONS-M21 scFv fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW04397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW04397 standard; Protein; 269 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                                                                                                                                                                                                                                                                                                                  Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 VSS 123
The present sequence is a scFv fragment from the chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAb, with human light and heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols. was
                                                                                                                                                                                                                         18-OCT-1994;
19-NOV-1993;
                                                                                                                                                                                                                                                                                                         JP08169900-A.
                                                                                                               Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
                                                                                                                                                               N-PSDB; AAT38662.
                                                                                                                                                                                                                                                             18-NOV-1994;
                                                                                                                                                                                                                                                                                   02-JUL-1996
                                                                                            Example 6; Pages 40-41; 45pp; Japanese
                                                                                                                                                                                                  (CHUS ) CHUGAI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                      94JP-0252166
                                                                                                                                                                                                                            93JP-0291078
                                                                                                                                                                                                                                                             94JP-0285057
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                                                                                                                                                                                                                                                                                                                                                                                            140..154
                                                                                                                                                                                                                                                                                                                                 /label= FLAG
                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                    155..261
                                                                                                                                                                                                                                                                                                                                                                              /label= linker
                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                          /label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.8%;
83.7%;
                                                                                                                                                                                                                                                                                                                                              269
                                                                                                                                                                                                                                                                                                                                                        "light variable region"
                                                                                                                                                                                                                                                                                                                                                                                                    "heavy variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 523; DB 16;
Pred. No. 1.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                       region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepd., and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain DNA mols. sepd. and connected with a peptide linker to produce a single stranded Fv region. The reshaped Fv region has low human antigenicity, and is therefore expected to be useful as an agent for the diagnosis and treatment of cerebral tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. myeloblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR81325 standard; Protein; 119 AA.
The sequence encodes the mouse antibody 21.6 heavy chain variable region, HC, directed against leukocyte adhesion molecule VLA-4. Cloned regions in the constance of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse by the amino acid present in the equivalent position of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanized VLA-4 antibody 21.6 heavy chain variable region, Hc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR81325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09519790-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-1994;
                                                                                                                                                                                                                                New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treatin
                                                                                                                                                                                                                                                                                     WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                                                   (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 vss 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VSS 123
                                                                                                                                                                                     Claim 13; Page 70; 105pp; English.
                                                                                                                                                                                                                                                                                                                    Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                    inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      94US-0186269
                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-US01219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.8%;
83.7%;
                                                                                                                                                                                                                                                                                                                         Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 523; DB 17;
Pred. No. 1.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                         Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                   Misc-difference
                                                                              Region
                                                                                                                   Region
                                                                                                                                                            Region
                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                        asthma; atheroscierosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia;
                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                               Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                              acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised alpha-4 integrin antibody 21.6 VH HC
                                                                                                                                                                                                                                                                                                                                                Chimeric
                                                                                                                                                                                                                                                                                                                                                          Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW22426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW22426 standard; Protein; 119 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and for treating inflammatory diseases such as multiple sclerosis. The meningities or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \tt qvqlvqsgaevkkpgasvkvsckasgfnlksyamhwvrqapgqrlewmgwinagngntky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vss 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                              Homo sapiens;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                 /note= "21/28'CL framework region 1" 27..30
/note= "21/28'CL Arg-72 is substd. by Ala of mouse 21.6 VL, important in supporting the CDR2
                                                                                                                 /note= "21/28'CL framework region 50..66
                                                                         /note= "21.6 complementarity determining region 67..98
                                         /note= "21/28'CL framework region 3"
                                                              /label= FR3
                                                                                                                                            /label= FR2
                                                                                                                                                             /note= "21.6 complementarity determining region
                                                                                                                                                                                                                             /note= "21/28'CL residues 27-30 are replaced by
                                                                                                  /label= CDR2
                                                                                                                                                                                 /label= CDR1
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                               /label= FR1
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82.9%;
                                                                                                                                                                                                           binding"
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Pred. No. 2.9e-40;
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                                                                                                                                                                                                                                                                    This polypeptide, designated Hc, comprises the heavy chain variable cregion (VH) of a humanised alpha-4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VH CZ cregion (see AAW22410) of mouse alpha-4 integrin monoclonal antibody CZ 1.6 and a modified human 21/28°CL framework. It contains an antibody CZ claimed humanised 21.6 VH version Ha (see AAW22412). Humanised CZ 1.6 VH and VL regions are used to produce claimed humanised CZ cantibodies useful in the manufacture of a medicament for treating CZ sthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory CX coversus host disease, tumour metastesis, nephritis, atopic mediated lung injury. The humanised antibodies have a half-life in the human circulation essentially equivalent to that of contribution covering the human set of the human circulation essentially equivalent to that of
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                                                                                                                                                                                                                                                                                           naturally occurring human antibodies
117 vss 119
                              121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uses of humanised alpha-4 integrin antibody - for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Fig 7; 107pp; English.
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                                                61 sqkfqgrvtitadtsastaymelsslrsedtavyycarggyfgs----gsnywgqgtlvt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ATHE-) ATHENA NEUROSCIENCES INC
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                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-NOV-1996;
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                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                   Local Similarity
                                                                                                            qvqlvqsgaevkkpgasvkvsckasgfniksyamhwvrqapgqrlewmgwinagngntky 60
                                                                                                                                                                                                                                                                119 AA;
                                                                                                                                                                                     Conservative
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/note= "21/28'CL framework region 4"
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82.9%;
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Pred. No. 2.9e-40;
5; Mismatches 12; Indels
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Search completed: May Job time: 247 sec

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OM protein - protein search, using sw model
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-561-521-9
US-08-561-521-4
PCT-USS5-01219-4
US-08-666-265A-132
US-08-646-265A-132
US-08-646-265A-132
US-08-646-265A-13
US-08-651-521-13
PCT-USS5-01219-13
PCT-USS5-01219-14
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US-08-232-081B-8
US-09-025-769B-36
US-09-025-769B-59
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US-08-137-117D-112
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PCT-US95-01219-11
US-08-561-521-17
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                                                                                                                                                                                                                                                                                                                                                                                                        Description
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sequence 17, Appl
sequence 17, Appl
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Sequence 86, Appl	Sequence 86, Appl	Sequence 86, Appl	•	•	3 6		л	53 •	53,	Sequence 53, APP1	-	л ·	74,	Sequence 23, Appl	Sequence 23, APPI	Sequence 16, Appl	,	9 ,	10.	110

ALIGNMENTS

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RESULT 1
US-08-561-521-11
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-561-521-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                    TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                           PILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
ADDRESSEE: Townsend and Townsend Khourie and Crew
ATRET: One Market plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                       FILING L... 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA: US/08/186,269A
APPLICATION NUMBER: US/08/186,269A
APPLICATION: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/561,521
                                                                 STRANDEDNESS:
                                                                                       TYPE:
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                                                                                     amino acid
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Query Match Best Local Similarity

100.0%;

Score 655; DB 2; Pred. No. 1.7e-58;

Length 123;

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PCT-US95-01219-11
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Humanized Antibodies Against Leukocyte NUMBER OF SEQUENCES: 45
                                                                                            / Match 100.0%; Score 655; DB 5; Length 123; Local Similarity 100.0%; Pred. No. 1.7e-58; Length 123; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran
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                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
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PCT-US95-01219-17

Sequence 17, Application PC/TUS9501219
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US-08-561-521-17
; Sequence 17, Application US/08561521
. patent No. 5840299
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/186
FILING DATE: 25-TAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                     140 VSS 142
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCES: 45
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                            61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Local Similarity 100.0%; Score 655; DB 2
Local Similarity 100.0%; Pred. No. 2e-58;
hes 123; Conservative 0; Mismatches
                                                                                                                                                                                                                                   20 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
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                                                                                                         Sequence 9, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 123; Conservative
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APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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                TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                          APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
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FILING DATE: 25-JAN-1995
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Local Similarity 100.0%; Pred. No. 2e-58;
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One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                       APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
MUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
ADDRESSEE: Townsend and Townsend Khourie and Crew
ADDRESSEE: Townsend and Townsend Khourie and Crew
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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STREET: Or
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                          121 VSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DPKFOGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGOGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                         STREET: Out ... CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94105
                                                      94105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/186,269A
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US-08-561-521-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Humanized Antibodies Against Leukocyte Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER: 15;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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                                                               FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 84.3%; Score 552; DB 5; Length 123; Local Similarity 82.9%; Pred. No. 3.3e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/
FILING DATE: 25-JAN-1995
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                                                                                                                                                                                                                                                      San Francisco
                                                                                                                                                                                                         94105
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5840299
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PCT-US95-01219-4
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                TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
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                                          TELEPHONE: 415-543-9600
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (
FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                        SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SaÍdanha, Jose
APPLICANT: Jones, S. Tarran
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            TELEPHONE: 415-543-5043
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ATTORNEY/AGENT INFORMATION:
NAME: SMITH, WILLIAM L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15
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                                                                          REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/01219 FILING DATE: 25-JAN-1995
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Leger, Olivier J.
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                                                                                                                                                   US 08/186,269
                                                                                                                                                                                                                                          Release #1.0, Version #1.25
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US-08-646-265A-132
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                                                       INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO PCT/JP94/01763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: RESHAPED HUMAN ANTIBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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TOPOLOGY:
                           TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                      NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3000 K St
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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3000 K Street, N.W., Suite 500
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                                                                                                                         (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
              protein
                                                                                                                                                                                                                                                                                                                                               09-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESHAPED HUMAN ANTIBODY TO HUMAN
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                                                                                                                                                                                                                                                     JP 5-291078
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                                                                                            132:
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                                                                                       US-08-646-265A-99
Query Match
Best Local S
Matches 103
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                                                                                                                                                                                            TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA
                                                                                                        MOLECULE TYPE:
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PIFILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN TITLE OF INVENTION: MEDULLOBLASTOMA CELLS NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                               TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 VSS 117
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y Match 79.8%;
Local Similarity 83.7%;
hes 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08 FILING DATE: 09-SEP-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                NAME: WEGNER, Harold C
REGISTRATION NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 114
                                                                                                                          TOPOLOGY:
                                                                                                                                            TYPE:
                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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    Application US/08646265A
    6214973

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                                                                                                                                     amino acid
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                                                                                                                                                                                                                             (202)672-5399
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                                                                                                                          linear
                                                                                                        protein
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83.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/646,265A
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Score 523; DB 4; Length 136;
Pred. No. 2.9e-45;
4; Mismatches 10; Indels
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Pred. No. 2.4e-45;
4; Mismatches 10;
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GENERAL INFORMATION:
                                                                                                                                         Matches
                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 5-2910
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 53.258
REFERENCE/DOCKET NUMBER: 5346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/646,265A FILING DATE: 09-SEP-1996 CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN TITLE OF INVENTION: MEDULLOBLASTOMA CELLS NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO PCT/JP94/01763 FILING DATE: 19-OCT-1994 PRIOR APPLICATION DATA:
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APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
                                                                                                                                                                                                                                       TOPOLOGY: Jin-
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                                '61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
83 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 136
                                                                  23 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                       103;
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                                                                                                                                                                                                                                                                                        269 amino acids
                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                          (202)672-5399
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                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: JP 5-291078
19-NOV-1993
                                                                                                                                                    79.8%;
83.7%;
                                                                                                                                Score 523; DB 4; Length 269; Pred. No. 6.5e-45; 4; Mismatches 10; Indels
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RESULT 13
PCT-US95-01219-13
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US-08-561-521-13
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; MOLECULE TYPE: protein US-08-561-521-13
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SEQUENCE CHARACTERISTICS:
FENGTH: 119 amino acids
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08561521 Patent No. 5840299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/186,269A FILING DATE: 25-JAN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Humanized Antibodies Ag
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
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117 VSS 119
                                    121 VSS 123
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                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, William L. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60
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Jones, S. Tarran
                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                              78.6%;
82.9%;
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                                                                                                                                                                                                                                            Score 515; DB 2; Length 119; Pred. No. 1.6e-44;
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US-08-561-521-12
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TOPOLOGY: linear;
MOLECULE TYPE: protein
PCT-US95-01219-13
                                                                                                                          Sequence 12, Application US/08561521 Patent No. 5840299
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 102;
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                                                                                                          GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application PC/TUS9501219 GENERAL INFORMATION:
 APPLICANT: Saldanha, APPLICANT: Jones, S. TITLE OF INVENTION: TITLE OF INVENTION:
                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
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APPLICANT: Jones, S. Tarran
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                                                                                                                                                                                                                                                                                        STREET:
CITY: Sa
STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 25-JA
                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                  Bendig, Mary M.
Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Humanized Antibodies Against Leukocyte Adhesion Molecule VLA-4
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82.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 515; DB 5; Length 119; Pred. No. 1.6e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
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RESULT 15
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                                                                                                                                                                                                                                                            Sequence 12, Application PC/TUS9501219 GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM
                                                                      TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                 APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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APPLICATION NUMBER: US/C
FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                  121 VSS 123
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                                                                 STREET: One Market I
                                COUNTRY:
                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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82.9%;
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; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-12
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PRIOR APPLICATION UNMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, William L.
REGISTRATION NUMBER: 15270-14
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-543-9600
TELEFAX: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              Query Match 78.2%; Score 512; DB 5; Length 119; Best Local Similarity 82.9%; Pred. No. 3.1e-44; Matches 102; Conservative 4; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01219

FILING DATE: 25-JAN-1995
117 VSS 119
                                      121 VSS 123
                                                                       CLASSIFICATION:
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Search completed: May 7, 2002, 12:23:04 Job time: 175 sec

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OM protein - protein search, using sw model
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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A47271
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248.659 Million cell updates/sec
   Ig heavy chain V r
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g heavy chain V-D
g heavy chain V-I
g heavy chain V r
g gamma chain V r
g gamma chain V r
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433 66.1 127 2 PH0955 433 66.1 135 2 PH0953 431 65.8 126 2 144151 429.5 65.6 108 2 PH1012 429.5 65.5 125 2 PH0957 427.5 65.3 143 1 E1HUND 427.6 5.2 125 2 S68170 427.6 5.2 125 2 S34014 428 64.9 129 2 S36260 429 64.8 147 2 PH1561 421 64.8 147 2 PH1561 421 64.8 171 2 S38250 421 64.3 246 2 S40295 420 64.1 121 2 S20783 420 64.1 121 2 S20783 421 64.3 165 2 PH1426 420 64.1 121 2 S20783 421 64.3 165 2 PH1426 420 64.1 121 2 S20783
127 2 PH0955 Ig 136 2 PH0953 Ig 126 2 I44151 Ig 108 2 PH1012 Ig 108 2 PH1012 Ig 127 2 PH0957 Ig 143 1 E1HUND Ig 129 2 S368170 Ig 129 2 S34014 Ig 129 2 S34014 Ig 129 2 S36260 Ig 147 2 PH1561 Ig 147 2 PH1561 Ig 147 2 PH1561 Ig 147 2 PH1561 Ig 146 2 S38950 Ig 147 2 F11426 Ig 148 2 S40295 Ig 149 2 S30783 Ig 140 2 S40295 Ig 141 2 S40295 Ig 142 2 S40295 Ig 143 1 S40295 Ig 144 1 S40295 Ig 145 1 S40295 Ig 146 2 S40295 Ig 147 2 PH1426 Ig 148 1 S40295 Ig 149 1 S40295 Ig 149 1 S40295 Ig 140 1 S40295
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chain V r

ALIGNMENTS

Ig gamma chain (WM65) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 C;Accession: S29594 A; Reference number: S29593 A; Accession: S29594 submitted to the EMBL Data Library, February 1991 RESULT C; Keywords: immunoglobulin A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591 A; Molecule type: mRNA A; Residues: 1-178 <SEY> A; Status: preliminary QY 밁 QΥ 밁 A;Molecule type: mRNA A;Residues: 7-120 <ROC1> A;Residues: 7-120 <ROC1> A;Cross·references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983 A;Otte: this sequence was determined from the differentiated gene A;Note: this sequence was determined from the differentiated gene R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug J. Immunol. 129, 2554-2558, 1982 R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, EMBO J. 2, 867-872, 1983 C;Species: Mus musculus (house mouse) C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000 C;Accession: S03471; S07453 밁 A; Reference number: S03471; MUID:84057768 A; Accession: S03471 A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-S03471 hypervariable regions. Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment) RESULT Matches Query Match Best Local 129 VSS 131 121 VSS 123 74 DPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG----GNY-AYGMDYNGQGTSVT 128 61 DPKFQGRVTITADTSASTAYMELSSLKSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120 N 93; Similarity Conservative 74.6%; Score 488.5; DB 2; 75.6%; Pred. No. 9e-37; 11; Mismatches 14; Indels Length 178; 5 Gaps 2;

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R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
                                                                                     Ig heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. BMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448
A;Accession: S36256; MUID:93178448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      If heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
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A; Residues: 1-43 <ROC2>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
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A:Accession: S07453
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                                                                                                                                                                                                                                                                               113 LVTVSS 118
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                                                                                                                                                                                                                                                                                                                                                                     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE----GYYGNYGVYAMDYWGQGT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.3%; Score 473.5; DB 2; 76.2%; Pred. No. 1.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.8%; Score 477; DB 2; 75.6%; Pred. No. 6.3e-36;
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R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
                                                                               Ig heavy chain V region (EB) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: S17586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-142 <LAR>
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A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybriddma cells A;Reference number: A2483; MUID:89273586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region - human (fragment)
c;Species: Homo sapiens (man)
c;Date: 12-oct-1989 #sequence_revision 12-oct-1989 #text_change 16-Aug-1996
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A;Accession: D33548
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73.2%;
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Pred. No. 5.9e-35;
8; Mismatches 22;
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60, 1250-1256, 1989
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Pred. No. 4.1e-35;
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A;Cross-references: EMBL:x60683; NID:g51820; PIDN:CAA43095.1; PID:g51821 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin f;15-98/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-117 <MYL>
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A;Accession: S17586
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06823
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID: 90064531
A;Accession: S06823
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Best Local
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                                    Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
C;Accession: PH0954
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  R; Martin,
J. Exp. M
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Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J. Exp. Med. 175, 983-991, 1992
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A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: pH0952; MUID:92202880
A;Accession: pH0954
A;Status: nucleic acid sequence not shown
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F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
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A; Residues: 1-132 < MAR>
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C:Species: Musculus (house mouse)
C:Date: 20-Feb-1995 *sequence_revision 20-Feb-1995 *text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of
A;Reference number: $24287
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A;Rosidues: 1-116 <MON>
A;Rosidues: 1-116 <MON>
A;Rosidues: 1-116 <MON>
A;Cross references: EmbL:X62705; NID:g51690; prDN:CAA44584.1; pID:g1333963
A;Cross references: preliminary
C;Status: preliminary
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A;Status: prelimina
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                                                                                                                                                                                                                                                                                                                     QY
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 YWGQGTLVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR------EGYYGNYGVYAMD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AQXFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARPHASIDDFWSGYYPNYYYYGMD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                   114 VSS 116
                                                                                                                                                                                      121 VSS 123
                                                                                                                                                                                                                                                          62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         2 VOLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.5%; Score 455; DB 2; Length 116; nilarity 71.5%; Pred. No. 5.7e-34; Conservative 13; Mismatches 14; Indels
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72.0%;

    Mismatches

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Pred. No. 4.8e-34;
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S49220

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                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <FIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Figini, M.; Marks, J.D.; Winter, G:; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: $46590; MUID:94254092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46393
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S46393
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A;Experimental source: strain Balb/c
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;121-221/Domain: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: immunoglobulin
F;1-120/Domain: V region #status predicted <VRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, September 1994
A.Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
A:Reference number: $49220
A:Accession: $49220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-221 <KIP>
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C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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121 KGTTVTVSS 129
                                         115 QGTLVTVSS 123
                                                         61 AQKFQGWYTMTRDTSISTAYMELSRLRSDDTAVYYCARDSAYYYDSSGYYSANYYMDVWG 120
                                                                                 61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREG--YYGNYGVYA----MDYWG 114
                                                                                                                                      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60
                                                                                                                                                                             1 OVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVKLLESGAELVKSGASVKLSCTASGENIKDTYMHWVKORPEQGLEWIGRIDPANGEIKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                       68.7%; Score 450; DB 2; Length 129; 70.5%; Pred. No. 1.8e-33; ative 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.5%; Score 455; DB 2; Length 221; 70.7%; Pred. No. 1.1e-33; ative 12; Mismatches 20; Indels
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A;Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <MAH>
                                                                                                                                                                                                                                                                                                                                                             R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                      A; Accession: S49530
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                                                                                           Matches 91; Conservative
                                                                                                                                                 Query Match
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A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not A;Reference number: S07453; MUID:83058021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 10-115 < ROC1>
A; Cross-references: EMBL: X03219
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A;Reference number: S03471; MUID:84057768
A;Accession: S03482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DPKFOGKATITTDTSSNTAYLQESSLTSEDTAVYYCARGTTVGR------DYWGQGTTLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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                                                                                                68.3%; Score 447.5; DB 2; Length 135; 72.8%; Pred. No. 3.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.5%; Score 449; DB 2; 70.2%; Pred. No. 1.9e-33;
                                                                              7; Mismatches
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                                                                            Indels 11;
                                                                    Gaps
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A;Variety: strain BALB/C
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03484; S07453
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S03484
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A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S07453; MUID:83058021
A; Accession: S07453
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A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: this sequence was determined from the differentiated gene
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A; Residues: 10-120 < ROC1>
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                                                                         R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0960
A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                  Ig heavy chain V region (G6+ T-L30) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0960
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A;Molecule type: DNA
A;Residues: 1-136 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-124/Region: complementarity-determining 3
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F;1-30/Region: framework 1
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Search completed: May 7, 2002, 12:23:48 Job time: 199 sec
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"The genetic basis of antibody production: the dominant anti-arsonate ridiotype response of the strain A mouse.";

RL Eur. J. Immunol. 12:1023-1033(1982).

C-1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER CONCLUDE THAT ALL OF THEST THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J RICEPTO; IPRO30306; Ig_MHC.

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                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Emammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
STRAIN=C57BL/6;
                          SEQUENCE FROM N.A.
                                                                          NCBI_TaxID=10090;
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MEDLINE=83144028; PubMed=6298778;
MECHAVI G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat)
IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
                                                                                NCBI_TaxID=9606
                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
-!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltimore D.;
                                                                                                                                                                                                                                                                                                                           80 NEKFKSKATLTYDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGS---SYFDYWGQGTTLT
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                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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77; Conserv
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Pred. No. 4.9e-34;
                                                                                                   Craniata; Vertebrata; Euteleostomi;
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JH2 SEGMENT
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Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Local Similarity 79.6%;
                                                                               EMBL; J00493; AAA38128.1;

PIR; A02028; HVMSG7.
InterPro; IPR003006; I9_MHC.
InterPro; IPR003596; I9_V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.";
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                                                Pfam; PF00047; ig; 1.
             SM00406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.
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             IGV; 1.
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pred. No. 9e-34;
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SEQUENCE
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SIGNAL 1 19
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01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V-I REGION V35 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV1G_HUMAN
                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. There are no restrictions on the the European Bioinformatics Institute. There are no restrictions on the two profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q., Ohno H., Fukuhara S., Honjo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 7:1047-1051(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Dispersed localization of D segments in the human immunoglobulin heavy-chain locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88296408; PubMed=2841108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Pfam; PF00047; ig; 1.

SMART; SM00406: IGV; 1.

Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                             EMBL; X07448; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                               PIR; S00476; HVHU35
                                                                                                                                                SEQUENCE
                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                         Interpro; IPR003006; Ig_MHC.
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                                                                                                                                                                NON_TER
                                                                                                                                                                                CHAIN
20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGRINPNSGGTNY 79
                             1 OVOLVOSGAEVKKPGASVKVSCKASGFNIKDTVIHWVRQAPGORLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity
75; Conserv
                                                                 1 Similarity
77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
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140
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                                                                                                                                                117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
                                                                  Conservative
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78.6%;
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                                                                                                                                                                                     IG HEAVY CHAIN V-I REGION V35
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                                                                                        Score 396; DB 1;
Pred. No. 7.1e-33;
                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA.
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                                                                                                       DB 1; Length 117
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HV1A_HUMAN
ID HV1A_H
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Best Local Similarity
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     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION J558
                                                                                          MOUSE
                                                                            HV13_MOUSE
                                                                    P01757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A02023; G1HUEU.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                              115 VSS 117
                                                                                                                                                                        121 VSS 123
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                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
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SMART; SM00406; IGV; 1.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gall W.E., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=71064027; PubMed=4923144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Picchemistry 9:3161-3170(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P01742;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V-I REGION EU.
                                                                                                                                                                                  61 AOKFOGRYTITÄDESTNTÄYMELSSLRSEDTÄFYFCA-----GGYGIYSPEEY-NGGLYT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFIDE BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=71064024; PubMed=5489771;
                                                                                                                                                                                                          61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HV1A_HUMAN
                                                                                                                                                                                                                                                    1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
  musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 AQKFQGRVTSTRDTSISTAYMELSRLRSDDTVVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemistry 9:3188-3196(1970).
MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
                                                                                                                                                                                                                                    QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPNY 60
                                                                                                                                                                                                                                                                                                       84;
                                                                                                                                                                                                                                                                                                                                                       22 96
117 117
117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;
(Mouse).
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                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                            59.5%;
                                                                                                                                                                                                                                                                                              8; Mismatches
                                                                                                                                                                                                                                                                                                     Score 390; DB 1; Length 117; Pred. No. 2.8e-32;
                                                                           PRT;
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                                                                        117 AA
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HV51_MOUSE
ID HV51_MOUSE
AC P06330;
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             SEQUENCE
                           NON_TER
                                     DISULFID
                                                     DOMAIN
                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                      Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes.";
                                                                 NIAMOC
                                                                               DOMAIN
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                             01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION AC38 205.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin v region.
DISULFID 22 96
                                                                                       Immunoglobulin V region.
                                                                                                                                                                                                                      MEDLINE=84182519; PubMed=6201362;
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 VSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schilling J., Clevinger B., Davie J.M., Hood L.;
"Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NOKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY-----WYFDVWGAGTTVT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=80078170; PubMed=6765983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120 : | | | | | | | | | 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                            A02040; MHMS38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, WHICH OCCUR IN THE D AND J SEGMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
          118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
117
117 AA;
                                                               99
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12934 MW; 94F7BEE4C762A018 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.7%; Score 378; DB 1; Length 117; 58.5%; Pred. No. 4.4e-31;
                           D SEGMENT.
J SEGMENT.
BY SIMILARITY.
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                                                                     V SEGMENT.
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RRESULT 10
HV12_MOUSE
ID HV12_MO
AC P01756
DT 21-JUL
DT 21-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 16 HEARY
OC Eukary
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OC Mammal
OX NCBL_I
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RN (1]
RN (1)
ROMEDLIN
RN KEhry
OC -1- M
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Best Local 9
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION MOPC 104E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heavy chain constant region domains.";
Biochemistry 21:5415-5424(1982).
-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HV12_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VSS 123
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MEDLINE=83075344; PubMed=6816276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete amino acid sequence of a mouse mu chain: homology among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocal
  115 VSS 117
                                                       121 VSS 123
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                                                                                                                                                                                                               1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60
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                                                                                                                                                                                                                                                                                                                                                  h 56.9%; Score 373; DB 1; Length 117; Similarity 59.3%; Pred. No. 1.4e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
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55
117
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                    19; Mismatches
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RESULT 11 HV11_MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way made by another the statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=81234548; PubMed=6788376;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J00539; AAA38172.1; -. PIR; A02038; G2MS43.
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SEQUENCE
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P03980;
23-OCT-1986 (Rel. 02, Created)
                                               HV48_MOUSE
                                                                                                                                                                             135 VSS 137
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                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                        80 NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARY-RLGRY----FDYWGQGTTLT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVOLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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54
68
85
117
117
137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.7%; Score 3/1.
60.2%; Pred. NO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 371.5; DB 1; Length 137; Pred. No. 2.4e-30;
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RESULT 13
HV50_MOUSE
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        EMBO J. 3:51/-02017-
PIR; A02037; MHMS15
            MEDIINE-84182519; PubMed-6201362; Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.; "A V region determinant (idiotope) expressed at high frequency in lymphocytes is encoded by a large set of antibody structural genes EMBO J. 3:517-523(1984).
                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION AC38 15.3.
     InterPro;
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                         Mus musculus (Mouse)
                                                                                                  SEQUENCE
                                                                                                                                                                                                                            P06329;
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                   135 TFSA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Illegitimate recombination generates a class switch from C mu to delta in an IgD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
PIR; A02033; HVMST7.
                                                                                                                                                                                                                                                                                                                                       80 NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDGYYDWF-----VYWGQGTLV 134
                                                                                                                                                                                                                                                                                                                                                              61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=84248078; PubMed=6429663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-1986 (Rel. 02, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                         20
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                               1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                        OVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY 79
IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15576 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.3%; Score 369; DB 1; Length 138; 58.1%; Pred. No. 4.2e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Mismatches
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                                                                                                                                                                                                                                120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Indels
                              structural genes.";
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                                                                                                                                                     SEQUENCE
                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
NON_TER 121 121
                                                                                                                                                                                                                                      Zakut R., Cohen J., Givol D.;
nucleic Acids Res. 8:4839-4840(1980).
-!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                        InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the cDNA corresponding region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin v region.
DOMAIN 99 105
DOMAIN 99 105
DOMAIN 106 120
                                                                                                                                                                                                                                                                                                      REVISIONS
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-81053741; Pubmed=6253904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION MPC 11.
61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                         1 EAGLOOSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY
                                              1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDDANGYTKY 60
                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P01745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HV01_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NEKFKSKATLTVDKSSSATYMQLSTPTSEDSAVYYCARWDYEGD----RYFDVWGTGTTVT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVQLLQPGTELVKPGASVNLSCKASGYTFTSYWHHWIRQRPGQGLEWIGGINPSNGGTNY 60
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                                                                                                                                                    121 AA;
                                                                                  Conservative
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99
106
22
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                                                                                                                                        13135 MW; 227AEF3EC56ED0BF CRC64;
                                                                                            55.0%;
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                                                                                23; Mismatches
                                                                                                Pred.
                                                                                         Score 360; DB 1;
Pred. No. 2.9e-29;
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Pred. No. 1e-29;
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Search completed: May 7, 2002, 12:32:34
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    PIR; A02042; HVMSB1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunglobulin V region; Signal.
SIGNAL
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 HEAVY CHAIN V REGION BCL1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-8222262; PubMed-6806821;
Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HV15_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by two adjacent CH genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 VSS 121
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                           134 VSS 136
                                                                                                      121 VSS 123
                                                                                                                                    61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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136
136 AA;
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136
15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                          55.0%; Score 360; DB 1; Length 136; 56.9%; Pred. No. 3.3e-29;
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OM protein - protein search, using sw model
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Perfect score:
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Maximum DB seq length: 2000000000
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655
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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1 Q99L31
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1 Q9Z1C4
1 Q9ZXF0
1 Q9QXF0
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1 Q99LC4
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      Q99LA6
Q9JL75
Q9JL77
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                              Q9d814 mus musculu
Q9d815 homo sapien
Q9u189 homo sapien
Q99125 mus musculu
Q9qxe9 mus musculu
Q9y298 homo sapien
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Q9z1c4 mus musculu
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Q9u194 homo sapien
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Q9yx2 schistosoma
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41.8 41.4	42.6	43.6	43.7	43.7	44.0	44.3	45.4	45.9	46.4	47.5	47.9	48.8	48.9	49.2	49.2	49.7	49.8	50.8	51.0	51.6	52.3	56.7	
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Q9rla4 mus musculu Q9j179 mus musculu	Snw	Q9bul0 homo sapien	oryc	09bqb8 homo sapien	09ul91 homo sapien	09n0w4 oryctolagus	09ul73 homo sapien	09u184 homo sapien	099ng4 mus musculu	09ul71 homo sapien	homo	home	homo	09u172 homo sapien	homo	Omo	mus		OMO		mus		09il81 mus musculu

ALIGNMENTS

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01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-JUN-2001 (TIEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9UL92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                          fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                               Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                     EMBL; AF035022; AAD56258.1; -.
InterPro; IPR003006; Ig_MIC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; if; i.
SMART; SM00406; IGV; i.
                                                                                                                                                                                                                                                                                                                                                                     Young D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                  Myosin-reactive autoantibodies in rheumatic carditis and normal
1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60
                                                                          1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                             DOMAIN.
                                                                                                          91;
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                                                                                                                                                                             124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;
                                                                                                          Conservative
                                                                                                                                                                                                124
                                                                                                          ; Score 457.5; DB 4; Length 124; pred. No. 5.1e-40; 9; Mismatches 16; Indels 15
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                           SEQUENCE
                                                                                                                                                                                                                                                  Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                         SMART; SM00406; IGV; 1.
                                                                                                                                     EMBL; AF206021; AAF69319.1; InterPro; IPR003006; Ig_MHC. IPR003596; Ig_v.
                                                                                                                  Pfam; PF00047; ig; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9JL85;
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submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DPKFQGRYTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLYT 120
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                      109 AA;
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11944 MW; DFE615FE6CED4EDE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 440; DB 11;
Pred. No. 1.7e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                              Query Match
              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TIEMBLIel. 17, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
                                                                    Q9GYZ2;
                                                                                 Q9GYZ2
                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
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                                                                                                                                                117 VSS 119
                                                                                                                                                                        121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin.
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF035020; AAD56256.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=98277139; PubMed=9614934;

Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
                                                                                                                                                                                  61 AQKFQGKYTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLW----FDPWGQGTLVT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                         61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UL94;
                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9UL94
                                                                                                                                                                                                                                    1 EVOLVESGAEVKKEGASVKVSCKASGYTFTGYYMHWVRQAEGGGLEWMGWINENSWTTNY 60
                                                                                                                                                                                                                                                 1 AELVKPGASVKLSCTASGENIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA 60
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                                                                                                                                                                                                                                                                                                     87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunol. Immunopathol.
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                                                                                                                                                                                                                                                                                                                                                       119 AA; 13205 MW; 13E64F5345F4A16E CRC64;
                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               119
                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                66.0%; Score 432; DB 4; Length 119; 70.7%; Pred. No. 2.1e-37;
                                                                                                                                                                                                                                                                                         10; Mismatches
                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Mismatches
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                                                                      119 AA.
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                                                                                                                                                                                                                                                                                        22; Indels
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Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schistosoma japonicum (Blood fluke).
Schistosoma japonicum (Blood fluke).
Bukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; 19; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
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Interpro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Q9UL95;
01-MAY-2000
                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                           Young D.C.
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                       121 VSS 123
                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NOKEKDRYTMTTDKSFSTAYMDLRSLKSADSAVYYCAR--YYDDH--YCLDYWGOGTTYT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                          NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGORLEWMGRIDPANGYTKY 60
                                                                EMBL; AF035019; AAD56255.1; --
                                                                                                        Clin. Immunol.
                                                                                                                                Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OVOLVESGAEVRKPGASVKVSCKASGYTFTGYYMNWVRQAPGHGLEWIGYINPSRGYTNY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                         -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                      fetus.
         InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                VSS 119
                                                                               DOMAIN.
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IPR003596; I9_v.
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                                                                                                                                                         Liu B., Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 AA;
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                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                            Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13567 MW; BA893873FD5FA6AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig.
Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.3%; Score 428; DB 5; Length 119; 66.7%; Pred. No. 5.5e-37;
                                                                                                                                                               der Merwe P.L., Kalis N.N., Berney S.M.,
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                                                                                                                                                                                                                                                                                                                                         125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Indels
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RP STRAIN=C57BL/6J; TISSUE-PANCREAS;

RC STRAIN=C57BL/6J; TISSUE-PANCREAS;

RC MEDLINE=21085660; PubMed=11217851;

RA KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Kawai J., Shinagawa A., Shibata K., Kondo S., Yamanaka I.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,

RA Arakawa T., Hara A., Fukunishi Y., Bono H., Kasukawa T., Saito R.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Aizawa K., Izawa M., Nishi Y., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Kaniya B., Kochiwa H.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,

RA Blake J., Boffelli D., Hofmann M., Hume D. A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
SEQUENCE
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AQKVQGRVTMTRDTTISTAYMELSRLRSDDTAVYYCARSQGGGRIAAAGDAFDIWGQGTM 120
                 InterPro; IPR003596; I9_v.
pfam; PF00047; 19; 4.
pfam; PF000409; IG; 2.
SMART; SM00409; IGC1; 3.
SMARR; SM00406; IGV; 1.
SMARR; SM00410; IG_like; 1.
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                                                                                                                                                                                                                                                                             EMBL; AK007918; BAB25349.1; MGD; MGI:1924014; 1810060005
                                                                                                                         InterPro; IPR003599; Ig-cl.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003606; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                             DOMAIN.
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125 AA;
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        PS00290; IG_MHC; UNKNOWN_1
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13516 MW; 0D3CD5C232488EAC CRC64;
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Last annotation update)
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                                                                                                                                                                                             DЬ
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UL89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                    EMBL; ARD35025; AAD56261.1; ...
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
NON_TER
                                                                              Q99L25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UL89; PRELIMINARY;
Q9UL89; PRELIMINARY;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
Homo sapiens (Human).

""""" Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                fetus.",
Clin. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                   61 OGRVTÍTÁDKSTSTAYMELSSLRSEDTAVYYCÁS----SNWGPYWYFDLWGRGTLVTVSS 116
                                                                                                                                 65 QGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY-AMDYWGQGTLVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                1 VOSGAEVKKPGSSVKVSCKASGGTFSSYAISWVROAPGQGLEWMGRIIPILGIANYAOKF 60
                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                     9
                                                                                                                                                                               5 VOSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGORLEWMGRIDPANGYTKYDPKF 64
                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 VSA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGY--DYDWFA--YWGQGTLYT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                         87;
                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                          116 116
116 AA; 12605 MW; C8F9131DE13EA898 CRC64;
                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                      62.8%; Score 411.5; DB 4; Length 72.5%; Pred. No. 2.8e-35; ative 3; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.4%; Score 422; DB 11; Length 473; 65.9%; Pred. No. 1.3e-35;
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Mismatches 19; Indels
                                                                 473 AA.
                                                                                                                                                                                                                                            DB_4; Length 116;
                                                                                                                                                                                                                  5; Gaps
                                                                                                                                                                                                                  2;
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Qγ
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                                                                                                     В
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                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                             EMBL; AJ225174; CAB65237.1; ...
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 VSS 117
                                                                                                                                                                                                                                                                                                                                                              090xE9;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                          121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                            61 NOKFKGKATLTVDKSSSTÄYMQLNSLTSEDSAVYYCÄRDRY-----YAMDYWGOGTSVT 114
                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                           1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9QXE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 ITVSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888 1; -
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 VTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 NEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGGSIYYG-YGLYYFDYWGQGTT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 QVQLQQSDAELVKPGASVKISCKVSGYTFTDHTIHWVKQRPEQGLEWIGYIYPRDGSTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QVQLVQSGAEVKKPGASVKVSCKASGENIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79;
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                         62.1%; Score 407; DB 11; Length 117; 62.6%; Pred. No. 8.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.4%; Score 408.5; DB 1 63.2%; Pred. No. 3.2e-34;
                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 25; Indels
                                                                                                                                 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 473;
                                                                                                                             6;
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Q9Y298
ID Q9Y
AC 09Y
AC 09Y
DT 01-
DT 01-
DT 166
GN 166
GN 166
GN 166
GN KHOM
OC Mamm
OX NCB
RN SEO
CRX MED
RP SEO
CRX MED
T 166
RT 166
RT 176
RP 116
RT 176
Q9BAVO
ID Q9BRVO
AC Q9BRVO
DT 01-UUN
DT 01-UUN
DT 01-UUN
DT 01-UN

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Best Local
                                                                                                                                                                                                                                                                                                                                                           Q9BRVO;
Q9BRVO;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
QNKNOWN (PROTEIN FOR MGC:14588).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
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Q9Y298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blood 92:496-506(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VIII inactivation: study with
IGG4 monoclonal antibody derived from a hemophilia A patient wit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGG VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=98322155; PubMed=9657749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC005951; AAH05951.1; -.
SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BRV0
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                           FISSUE=PROSTATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVP-----DPDAFDIWGQGTMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAPGKGLEWVGSFDPESGESIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AJ224083; CAA11829.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16031 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.9%;
                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 399; DB
Pred. No. 7.5e
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                      Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        563D164AB22802D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
.5e-34;
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RESULT
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Best Local Similarity
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Best Local
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
NON_TER 1
Q9QXF0;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 11, Last sequence update)
01-JUN 2001 (TrEMBLrel. 17, Last annotation update)
ANTI-PORCINE VCAM MAB 3P4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Humanized porcine VCAM-specific monoclonal antibodies with chimeric IgG2/G4 constant regions block human leukocyte binding to porcine endothelial cells.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/C;
Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A.,
Matis L.M., Evans M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9Z1C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9Z1C4
                                                                                Q9QXF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Si.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 GTTVTVSS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 GTLVTVSS 123
                                                                                                                                                                                                                    113 TLTVSS
                                                                                                                                                                                                                                                                      118 LVTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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                                                                                                                                                                                                                                                                                                                        61 TOKFRGKATLTADKSSSTAYMOLSSLASEDSAVYYCARRTVGGYF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                                                                                                                                                                                                                                                                                          DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE---GYYGNYGVYAMDYWGQGT 117
                                                                                                                                                                                                                                                                                                                                                                                                                              QVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 59.5
75; Conservative
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  (TrEMBLrel. (TrEMBLrel.
                                                                                  PRELIMINARY;
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Pred. No. 3.7e-33;
     Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 386.5; DB 1
Pred. No. 1.1e-32;
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                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                             -DYWGQGT 112
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Best Local
SEQUENCE
                                         Signal.
SIGNAL
NON_TER
                                                                                                                                                                                                                                                                                                   JOX A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M., Bohlen H., Diehl V., Wolf J.;
Bohlen H., Diehl V., Wolf J.;
"Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a patient with mixed cellularity Hodgkin's disease is associated with somatic mutations within the untranslated regions of rearranged and class switch recombinated Ig genes.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               095978;
01-MAY-1999 (TIEMBLIEL. 10, Created)
01-MAY-1999 (TIEMBLIEL. 10, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
VH1 PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                  SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                          EMBL; AJ005570; CAA06599.1; -.
                                                                                                                                                                                                                                                                       -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-PERIPHERAL BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-:- SINILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 TVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 TVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDKDYY------FDYWGQGTTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity hes 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ225171; CAB65236.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
           157
17304 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Mismatches
                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 386; DB 11;
Pred. No. 1.2e-32;
           86986EDDA84D88B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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136 VTVSS 140
                           119 VTVSS 123
                                                   80 AEKFQGRLTMTRNTSTTTVYMELSRLRFEDŢAVYFCGRGGRWRSGNYN----GHWGQGTP 135
                                                                61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYY--GNYGVYAMDYWGQGTL 118
                                                                                                                 20
                                                                                                                                                                                   Local Similarity
                                                                                                                           1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
                                                                                                          QVQLVQSGAEIKRPGASVKVHCKTSGYVFTSYYIHWVRQPRGQGLEWMGGIGPGVGSTMC 79
                                                                                                                                                                     Conservative
                                                                                                                                                                                58.6%; Score 384; DB 4; 63.2%; Pred. No. 2.8e-32;
                                                                                                                                                                    10;
                                                                                                                                                                    Mismatches
                                                                                                                                                                    30;
                                                                                                                                                                                             Length 157;
                                                                                                                                                                  Indels
                                                                                                                                                                  6;
                                                                                                                                                               Gaps
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Search completed: May 7, 2002, 12:31:42 Job time: 628 sec

2;

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OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                        Result
                                                                                                                                                                                                                                       No.
                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
634
619
618.5
569
539
539
535
530.5
                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    May 7, 2002, 12:18:19; Search time 67.39 Seconds (without alignments) 138.496 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A_Geneseq_1101:*
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                                                                                                                                                                                                                                         Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           // SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
// SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
// SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
// SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
// SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA199.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
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AAR81332
AAW22409
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AAR06252
                           AAY29911
AAY29916
                                                                                                                                                 AAR60627
        AAR78970
                                                                  AAY29913
                                                                                     AAR81328
                                                                                                                                                                                                                                                                                                           SUMMARIES
                                Humanised alpha-4
Variable region of
Mouse anti-VLA-4 a
Human MCP-3 and mu
Human IP-10 and mu
Artificial Synthet
                                                                                                                                                   Mouse VLA-4 antibo
Human VLA-4 reshap
Alpha-4 integrin m
ME1-14 light chain
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                 Light chain variab
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AABBI999	AARO40	20000	0807044	ACPF G G G	AAW24990		AAY		AAT			AARIAKU					AND 01010	MAN4 / 20 /	33847307	1000000	MAD01330	MAWIU200	AABolyy	AARLUOUS	AAR26981	AARLS658	AAW35133	AAK85495	AAW20/9/	AAWZ6600	AAKZOSO	AARYSIO	AAW2241	AAR8132	
	0	MAD SCH94.03 light	\sim	Mouse Caet to train	MOHOCIOHAL ANGLESIS		lonal anti	IGFA	acid sequ	Amino acid sequenc	ar	pXOM2. Mus muscul	Mouse MAD 1C11 L c	Anti-human CD23 5E	Ganglioside GD3 sp	Amino acid sequenc	Light (kappa) chai	Ganglioside GD3 sp	Human/murine IL-1	antibo	Humanized 1308F VL		TF8-5G9 CDR-grafte	Ganglioside GD3 sp	ecific	Ē	ine OKT4	ē	<u> </u>	MAb	₹	(FRP51)-ETA fusion	_	Humanized and ***	י ר

ALIGNMENTS

AAR81326 RESULT

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AAR81326;

23-MAR-1996 (first entry)

AAR81326 standard; Protein; 126 AA.

Mouse VLA-4 antibody 21.6 light chain variable region.

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Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                           antibody engineering.
                                                                                                                                Key
                                                                                                                                             Mus musculus.
                                                                                            Region
                                                                                                          Region
                                                                                                                        Peptide
                                                                             Region
                                                                Region
WO9519790-A1.
                      Region
                                    Region
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                                                                                /note=
55..69
                                                                                                           /note= "signal peptide" 21..43
                                                    /note=
77..10
                                                                  /note=
70..76
                                                                                                    /note= "framework region 1"
                                                                                                                                Location/Qualifiers
                        /note=
117..1
                                      /note= "framework region 3"
109..116
               /note= "framework region 4"
                                                    .108
                        ..126
                                                                                      "complementarity determining region 1"
                                                           "complementarity determining region
                              "complementarity determining region 3"
                                                                         "framework region 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Homo sapiens
                            antibody engineering.
                              Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                               Human VLA-4 reshaped antibody 21.6 light chain variable region.
                                                                                                                                                                         AAR81332 standard; Protein; 126 AA
                                                                                                                     23-MAR-1996
                                                                                                                                                                                                                                                                      121 tkleik 126
                                                                                                                                                                                                                                                                                                      121 TKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                   61 gkrprilihytsaiqpgipsrfsgsgsgrdysfnisnlepediatyyclqydnlwtfggg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ99889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                          N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1995-269276/35
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 680; DB 16; 100.0%; Pred. No. 1.2e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                     framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the antibodies can be used to inhibit adhesion of a leukocyte to an multiple sclerosis. They can also be used in the treatment of antibodies can be transaction and to treat inflammatory diseases such as stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity nurification or for meneration anti-laid-tune.
                                                                                                                                  The sequence represents the human reshaped antibody 21.6 light chain variable region against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892) of a regions are linked to human constant regions in the construction mouse cDNAs are modified using PCR primers (See AAQ99895-98) and mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR
 Sequence
            purification or for generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                            Disclosure; Fig 10; 105pp; English.
                                                                                                                                                                                                                                                                                                                            New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                           inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ99893
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-1994;
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126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0186269.
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77..10
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70..76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=_"complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                      Leger OJ, Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "complementarity determining region
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Qγ
                                 DЪ
                                                       Matches 126;
                                                                    Query Match
Local Similarity
                                                     Conservative
                                                       100.0%; Score 680; DB 16; 100.0%; Pred. No. 1.2e-47;
                                                     0;
                                                   Mismatches
                                                 Indels
                                                             Length 126;
                                                 0;
                                                Gaps
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SO XXX WXX DE XXX

В

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
This polypeptide comprises the light chain variable region (VL) mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VL can be
                                                         Uses of humanised alpha-4 integrin antibody - asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritts; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia;
                                                                                                                  Bendig
                                                                                                                                                                                                                                                        Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acute Leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-4 integrin mouse MAb 21.6 VL region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW22409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW22409
                                     Claim 18; Page 68; 107pp; English.
                                                                                                                                     (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                          21-NOV-1995;
                                                                                                                                                                            21-NOV-1996;
                                                                                                                                                                                                                   WO9718838-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TKLEIK
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                                                                                       1997-297879/27.
DB; AAT74759.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                   Jones
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                                                                                                                                                         95US-0561521.
                                                                                                                                                                            96WO-US18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                            /note=
55..69
                                                                                                                                                                                                                                                                                                                                                                                                        /note=
44..54
                                                                                                                                                                                                                                                                                                                   /label= CDR2
/note= "complementarity determining
77..108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                     /note= "framework region 4"
                                                                                                                                                                                                                                                         /note= "complementarity determining region
117..126
                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Leader
                                                                                                                                                                                                                                              'label=
                                                                                                                                                                                                                                                                          'label=
                                                                                                                                                                                                                                                                                              /note= "framework region
                                                                                                                                                                                                                                                                                                         /label= FR3
                                                                                                                                                                                                                                                                                                                                                                 /label= FR2
                                                                                                                                                                                                                                                                                                                                                                                               'label= CDR1
                                                                                                                   ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                      "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                "framework region
                                                                                                                                                                                                                                                                                                                                                                                    "complementarity determining region
                                                                                                                   Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                             FR1
                                                                                                                                                                                                                                                FR4
                                                                                                                                                                                                                                                                            CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126
                                                                                                                   Saldanha
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                                                                   for treatment
                                                                                                                   Yednock
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RESULT
AAR60627
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CCCXXXXIII
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Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            incorporated into a human REI framework to produce a claimed humanised 21.6 VL (see AAW2412) and a claimed humanised 21.6 antibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibodies of the invention have a half-life in the human circulation essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 equivalent to that of naturally occurring human antibodies.
                                                                     Method of treating solid or cystic tumours with antibodies -administering monoclonal antibody Mel-14, having Fc deleted, using injection or deposition in the cyst cavity
                                                                                                                                WPI; 1994-316669/39.
N-PSDB; AAQ73537.
                                                                                                                                                                          Bigner DD,
                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR60627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR60627 standard; Protein; 128
                                        Disclosure; Fig 2; 31pp; English.
                                                                                                                                                                                                      (BIGN/) BIGNER D D.
(CARR/) CARREL S.
(ZALU/) ZALUTSKY M R.
                                                                                                                                                                                                                                                                   19-MAR-1993;
                                                                                                                                                                                                                                                                                               14-MAR-1994;
                                                                                                                                                                                                                                                                                                                            29-SEP-1994
                                                                                                                                                                                                                                                                                                                                                          WO9421294-A
                                                                                                                                                                                                                                                                                                                                                                                                                                               ME1-14 light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 tkleik 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 mrpsigflglllfwlhgaqcdiqmtqspsslsaslggkvtitcktsqdinkymawyqhkp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRPSIQFLGLLLEWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gkrprllihytsalqpgipsrfsgsgsgrdysfnisnlepediatyyclqydnlwtfggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 AA;
                                                                                                                                                                            Carrel S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                   93US-0033864
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                                                                                                                                                                            Zalutsky MR;
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Pred. No. 1.2e-47;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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The sequence is that of the MEI-14 light chain. The protein monoclonal antibody which can be administered to treat solid

The

or

The sequence is that of the ME1-14 light chain.

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AAW22419
ID AAW2
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Best Local
W09718838-A1
                                                                                                                                                                                                                                                                                                                            Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastrasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia;
                                                                                                                                                   Region
                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                           Chimeric
                                                                                                                                                                                                                                                                                                     Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cystic tumours.
See also AAR60626.
                                                                                                                       Region
                                                                                                                                                                               Region
                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                    Chimeric
                                                                                                                                                                                                                                                                                                                     acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                        08-DEC-1997
                                     Region
                                                                 Region
                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                     Humanised alpha-4 integrin antibody 21.6 VL version La
                                                                                                                                                                                                                                                                                                                                                                                                                           AAW22419;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW22419 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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les 118; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tkleik 126
                                                                                                                                                                                                                                                                                  Homo sapiens;
synthetic.
                                                                                                                                                                                                                                                                                                     Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                     /label- CDR3
/note= "21.6 complementarity determining
117..126
                                                                   109.
                                                                        /label= FR3
/note= "REI framework region
                 /note= "REI framework region 4"
                                                                                                    /label= CDR2
/note= "21.6
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                               'note= "REI framework region
                                                                                                                                           'label= FR2
                                                                                                                                                           note= "21.6 complementarity determining
                                                                                                                                                                      /label= CDR1
                                                                                                                                                                                      note= "REI framework region
                                                                                                                                                                                                                /label= Mat_protein
/note= "VL version La (Claim 25)"
                                                                                                                                                                                                                                              /label= Leader
                                                                                                                                                                                                 'label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 126 AA
                                                                 .116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.2%;
93.7%;
                                                                                                  complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 634; DB 15;
Pred. No. 5.9e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                             region
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                                                                                                                                                                                                                                           AAR06252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This polypeptide, designated La, comprises the light chain variable cregion (VL) of a humanised alpha-4 integrin antibody 21.6 (see also AAW22412). It is composed of complementarity determining regions from the composed in mammalian host cells following pCR amplification and mutagenessis of appropriate mouse and human DNA sequences. The mutagenessis of appropriate mouse and human DNA sequences. The composed composed to produce a claimed humanised 21.6 vH (see AAW22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the manufacture of a medicament for treating asthma, atherosclerosis, and enentia, diabetes, inflammatory bowel disease, theumatoid composed transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial composed in the human circulation essentially antibody has a half-life in the human circulation essentially and cover equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                             EP380068-A.
                                                                                                                                                                                                                       AAR06252 standard; protein; 128
                                                                                        Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
                                                                                                                           Variable region of murine AHT
                                                                                                                                                           10-DEC-1990
                                                                                                                                                                                           AAR06252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uses of humanised alpha-4 integrin antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Fig 10; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                    GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                     gkaprllihytsalqpgipsrfsgsgsgrdytftisslqpediatyyclqydnlwtfgqg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atherosclerosis, AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones ST,
                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0561521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.0%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leger OJ, Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 619; DB 10,
Pred. No. 9.2e-43;
                                                                                                                       107 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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01-AUG-1990

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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
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24-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression vectors for producing chimeric monoclonal antibodies which express human constant region and non-human variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                        antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR THERAPEU
                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR81328;
                      Regior
                                                                                                                Region
                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse anti-VLA-4 antibody 21.6 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 gtklevr 127
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DB; AAQ05556.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity 88.1
112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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89US-0301216
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50..56
/label= CDR2
                                                                                                                     35..49
                                                                    /note=
                                                                                             /label=
                                                                                                                                                               /note=
                                                                                                                                                                                          -tabet
                                                                                                                                                                                                                                                            /note-
                                                                                                                                                                                                                                                                                    /label= FR1
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.0%;
88.2%;
                                                "mouse light chain region 2"
                                                                                                                                    "mouse light chain variable determining region 1"
                                                                                                                                                                                                                              "mouse light chain variable framework region 1"
                                                                                             FR2
                                                                                                                                                                                       CDR1
                                            region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 618.5; DB Pred. No. 1e-42; Mismatches
                                                                    variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 128;
                                                                                                                                                            complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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RESULT
AAY29913
ID AAY2

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AAY29913 standard;

Protein;

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61

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81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126

rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik

106

diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips

60

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Qy
                                                                                                                                                                    variable region (without signal sequence). Cloned cDNA CDR sequences of comouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and the 2*CL antibody for the heavy chain in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, CL58 and L69 in the human kappa LCVR framework are replaced by the amino cacid present in the equivalent position of the mouse 21.6 Ig light coll. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a cleukocyte to an endothelial cell and to treat inflammatory diseases such cas multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating
                                              Query Match
Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                            Sequence
                                                                                                                                                           anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 66; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-269276/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9519790-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
               21
                                             Local Similarity es 106; Conserv
DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MM,
                                                                                                                            106 AA;
                                           83.7%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0186269
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/label= FR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "mouse light chain variable framework
    region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "mouse light chain variable complementarity
    determining region 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "mouse light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "mouse light chain variable region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          determining
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                                              0;
                                              Score 569; DB 16
Pred. No. 8e-39;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain variable region 3"
                                                                             DB 16;
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                                              0;
                                                                             Length 106;
                                                Indels
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     DAX AX I
                                                                                      AAY29911
                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                       Matches 101;
                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HTV antigen. Specifically claimed fusion proteins comprise; (1) human monocyte chemotactic protein 3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human SDF-1 and human Muc-1; (5) human IP-10 and HIV pp120; (6) human MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV gp120. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays for identifying unknown tumour antigen epitopes and fine mapping of tumour antigen epitopes. The present sequence represents a fusion protein from the mapping of
17-NOV-1999 (first entry)
                                   AA $29911;
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 118-119; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9946392-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                                    AAY29911 standard; Protein; 361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MCP-3 and murine scFv38 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1999
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                                                                                                                                                                                                                      229
                                                                                                                                                                                                                                                                                                                                                                                                         from the present invention.
                                                                                                                                                       289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune response; HIV; infection.
                                                                                                                                                               77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                  17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
                                                                                                     9
                                                                                                                                                gipsrfsgsgsgrdysfsisnlepediatyyclgydnlytfgggtkleik 338
                                                                                                                                                                                                                 gsgsdigmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqp 288
                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biragyn A;
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                   79.3%;
                                                                                                                                                                                                                                                                                   Score 539; DB 20;
Pred. No. 6.7e-36;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                   Length 359;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                        AAY29916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes fusion proteins comprising a chemokine at unmour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human CC (Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human SDF-1 and human MCC-1; (5) human IP-10 and HIV 9p120; (6) human MCP-3 and HIV 9p120; (7) human MCC and HIV 9p120; and (8) human SDF-1 and HIV 9p120. The fusion proteins, and nucleotide sequences encoding them, can concerve the sequence of the sequence of the concerve that the sequence of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                Artificial synthetic construct protein SEQ ID NO:15.
                                                                                                                                                   AAY29916;
                                                                                                     17-NOV-1999
                                                                                                                                                                                                 AAY29916 standard; Protein; 374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 115-116; 142pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-551418/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                           infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human IP-10 and murine scFv38 fusion protein.
                                                                                                                                                                                                                                                                                                                 291 gipsrfsgsgsgrdysfsisnlepediatyyclgydnlytfgggtkleik 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                             77 GIPSRFSGSGSGRDYSFNISNLEPEDIATTYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.3%;
91.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 539; DB 20;
Pred. No. 6.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                           proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (3) human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV gp120. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays for identifying unknown tumour antigen epitopes and fine mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AAZ21168 are sequences given in the SEQ ID LISTING in the present invention but which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 117-118; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-551418/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kwak LW, Biragyn A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune response; HIV; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                     Synthetic
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                     Monoclonal antibody; heavy metal; mercury; variable region;
                                                                          Light chain variable region for monoclonal antibody 23F8.
                                                                                                 21-DEC-1995
                                                                                                                       AAR78970
                                                                                                                                            AAR78970 standard; Protein; 107 AA
                                                                                                                                                                                                  155 rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 200
                                                                                                                                                                                                             81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                            21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes fusion proteins comprising a tumour antigen or HIV antigen. Specifically claimed i
                                                                                                                                                                                                                                                                                                                                                                    not mentioned further within the specification.
                                                                                                                                                                                                                                                                                            100;
                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                            Conservative
                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                ξ
                                                                                                                                                                                                                                                                                                    78.78;
94.38;
                                                                                                                                                                                                                                                                                                    Score 535; DB 20;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                              DB 20;
                                                                                                                                                                                                                                                                                                              Length 374;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a chemokine
                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                            0;
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She and 328) were producing MADS that were strongly positive egainst glutatione-mercuric ions but negative against glutathione without mercuric ions. RNA was isolated from hybridoma cells with guanidine isothiocyanate. First strand coNA synthesis was catalysed by MALLY reverse transcriptese. The primers used for cDNA synthesis were complementary to the 5' end of the CHI domain of the havy chain expressed by the hybridoma of interest, or to the 5' and of the C kappa domain. Some of the primers used for cDNA synthesis are shown in AAO97511-097518. The primer used for cDNA synthesis of the crainable region of a particular antibody polypeptide was also used for cPR amplification of that variable region, in conjunction with an appropriate V-region primer. In addition, the VH primer AAO97518 was used to amplify the mAD 2D5 and 5B6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given in AAO97498-097510 and the deduced AA sequences in AAR97941-R79250 & AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are different from the descriptions in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neutralising heavy metals
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Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic
                                                                                                                               Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
                                                                                                                                                                                                                                                 02-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR81321 standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence listings. The descriptions in the sequence listings are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wagner FW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 AA;
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                                                                                                                                                                                                                                           (first entry)
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AAW22412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ends of the mouse cDNAs are modified using PCR primers (See AAQ9895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-l constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LC WR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmads encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and for treating inflammatory diseases such as multiple
Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                                        Humanised alpha-4 integrin antibody 21.6 VL La.
                                                                                                                             08-DEC-1997
                                                                                                                                                                                            AAW22412 standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence encodes the humanized mouse antibody 21.6 light chain variable region, La, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 67; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bendig MM, Jones TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1995;
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Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory disease.
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                                                                                                                                                                                                                                                                        21 DIQMTQSPSSLSASLGGKYTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                         1 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 AA;
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 74.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 508; DB 16; Length 106; Pred. No. 6.3e-34;
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Claim 25; Fig 6; 107pp; English.
                          Uses of humanised alpha-4 integrin antibody - asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                   Bendig MM,
                                                                                                                                                21-NOV-1996;
                                                            WPI; 1997-297879/27.
                                                                                                      (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                             21-NOV-1995;
                                                                                                                                                                      29-MAY-1997.
                                                                                                                                                                                            W09718838-A1
                                                                                                                                                                                                                                   Misc-difference 106
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                                                                                                                                                                                                                                                                                                  Misc-difference
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Chimeric Homo sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
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                                                                                  Jones ST,
                                                                                                                            95US-0561521
                                                                                                                                                96WO-US18807
                                                                                                                                                                                                                                                                                       103
/note= "REI Leu-103 substd. by Val,
                                                                                                                                                                                                                                                                                                                                                                                                           69
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                                                                                                                                                                                                                                                                                                                         97..106
/label- FR4
                                                                                                                                                                                                                                                                                                                                         /label= CDR3 /note= "21.6 complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                  89..96
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "REI Val-58 is substd. by Ile of mouse
21.6_VL, important in supporting the CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "21.6 complementarity determining region 2" 57..88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "21.6 complementarity determining region 1" 35..49
                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "REI Lys-45 is substd. by Lys of mouse 21.6~\mathrm{VL}, important in supporting the
                                                                                                                                                                                                                                                                                                           /note= "REI framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "REI framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "REI framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "REI framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= FR1
                                                                               Leger OJ,
                                                                                                                                                                                                          "REI Thr-106 substd. by Lys, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                         "REI Gln-104 substd. by Glu, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                           "REI Thr-69 is substd. by Arg of mouse 21.6 VL, involved in antibody-antigen binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "REI Tyr-49 is substd. by His of mouse 21.6 VL, located at the binding site"
                                                                                                                                                                                                                                                                           of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VL, important in supporting the loop"
                                                                               Saldanha J,
                                      for treatment
                                                                                Yednock TA;
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AAR93159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha 4 integrin antibody 21.6. It is composed of complementarity determining regions (CDRs) from the VL region (see AAW22409) of mouse alpha 4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be expressed in mammalian host cells following PCR amplification and mutagenesis of appropriate fragments of mouse and human DNA sequences. The humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used to produce a claimed humanised 21.6 antibody that is useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibody has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       manufacture of a medicament for treating asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour
          Region
                                                                                                                                                                                                                                                                          Antibody; light chain; kappa; variable region; K20; integrin; CD29; beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                half-life in the human circulation essentially equivalent to that of naturally occurring human antibodies.
                                                                                                                                                                           Region
                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                               T cell activation;
                                                                                                                                                                                                                                                                                                           Murine monoclonal antibody K20 kappa chain variable region
                                                                                                                                                                                                                                                                                                                                  24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                       AAR93159;
                                                                                                                                                                                                                                                                                                                                                                           AAR93159 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                61 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                           /note=
57..88
                                                                                                                                         /note=
35..49
          /label= CDR3
/note= "complementarity determining region"
95..108
                                            /note= "framework region"
89..94
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                /label= CDR1
/label= J_kappal
                                                                /label= FR3
                                                                                                 /label= CDR2
                                                                                                                     /note= "framework region
                                                                                                                                 /label= FR2
                                                                                                                                                                                    /note=
                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                               complementarity determining region; CDR
                                                                                                                                                                                                                                                                                                                                                                           Protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.7%;
                                                                                      "complementarity determining
                                                                                                                                                     "complementarity determining region"
                                                                                                                                                                                     "framework region"
                                                                                                                                                                                                FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 508; DB 18;
Pred. No. 6.3e-34;
                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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AAR26983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody K20. The antibody recognises the beta 1 subunit (CD29) of integrins and inhibits activation and proliferation of peripheral T cells induced by anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target for humanisation; the humanisation process, the complementarity determining regions (CDRs) of a human antibody with framework regions 70-95% homologous to those of K20 were replaced by the K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INRM )
(PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 2A; 39pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanisation of non-human immunoglobulin variable regions - prodn. of humanised antibodies, esp. K20, e.g. as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT26849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bernard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FR2724393-A1
                    Domain
                                                                                                                                                                                                                                                                                                                           11-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                      AAR26983;
                                                                                                                                                                                                                                                                                                                                                                                                              AAR26983 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-1996.
                                                                                                                                                                        Pseudomonas
                                                                                                                                                                                                                 Monoclonal antibody; light chain; heavy chain; tumour; c-erbB-2; variable region; ETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1mmunosuppressant
                                                               Peptide
                                                                                                                                                                                                                                                                                (FRP51)-ETA fusion protein
                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diqltqspsslsaslggkvtitckasqdinkyiawyqhepgkgprllirytsklesgips
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cervoni MF, Lefranc MP,
                                                                                                                                                                      aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                              Location/Qualifiers
                                                                                   /label=
                                        /label= FLAG_peptide_and_enterokinase_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.7%;
89.6%;
FWP51_heavy_chain_variable_domain
                                                                                   ompA_signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 508; DB 17;
Pred. No. 6.4e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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Peptide

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Search completed: May
Job time: 245 sec
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                                                                                                                                                            Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                          The sequences given in AAR26982-3 contain part of the exotoxin A (ETA) sequence corresponding to positions 252-613 of the full exotoxin A sequence. These sequences are encoded by Fv(FRP5)-ETA fusion genes. The ETA sequence was used as a marker gene so that E. coli transformed with the fusion gene could be identified. The fusion genes were expressed in E. coli and the antibodies were extracted. These recombinant antibodies can be used for the qualitative and quantitative determination of c-erbB-2. This can be used for monitoring or in-vivo localisation of tumours overexpressing c-erbB-2.
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 53-58; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Recombinant antibodies directed to growth factor receptor C-erbB-2 - for diagnosing and treating tumours expressing C-erbB-2 e.g. breast or ovarian tumours \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Groner B,
Zwickl M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ28263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-302096/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP502812-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                        Hardman N,
                                                                                                                                                                                                                           637 AA;
                                                                                                                                                             Conservative
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168..274
           7,
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                                                                                                                                                                      74.78;
           2002, 12:22:24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harwerth I, Hynes NE,
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                                                                                                                                                                     Score 508; DB 13; Length 637; Pred. No. 3.6e-33;
                                                                                                                                                            Mismatches
                                                                                                                                                            10;
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Result
No.
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
        Pred. No. score grea and is der
     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length: 2000000000
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                 Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_AA: *
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Listing first 45 summaries
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680
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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     106
107
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 US-08-561-521-2
US-08-561-521-5
PCT-US95-01219-15
US-08-339-582-4
US-08-361-521-5
PCT-US95-01219-5
US-08-888-366-22
US-08-861-521-7
PCT-US95-01219-7
PCT-US95-01219-7
US-08-235-838-16
US-08-235-838-11
US-08-465-4738-11
US-08-465-4738-11
US-08-465-4738-11
US-08-465-17-14
US-08-468-671-14
US-08-488-671-14
US-08-488-671-14
US-08-488-671-14
US-08-348-548-4
US-08-336-171
US-08-348-18-63
US-08-383-137-117D-37
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Sequence 2, Appli
Sequence 15, Appl
Sequence 2, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 11, Appli
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Sequence 2, Appli
Sequence 3, Appli
Sequence 63, Appli
Sequence 71, Appli
Sequence 37, Appli
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
410.5	410.5	412.5	413.5	413.5	413.5	413.5	414.5	416.5	416.5	417.5	417.5	417.5	418.5	418.5	423.5	424.5	426.5
60.4	60.4	60.7	60.8	60.8	60.8	60.8	61.0	61.2	61.2	61.4	61.4	61.4	61.5	61.5	62.3	62.4	62.7
128	127	127	127	125	125	125	128	127	127	127	127	127	142	142	236	127	127
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US-08-569-147-80	US-08-933-983-17	US-09-136-315-8	US-08-649-100-33	US-08-465-313-2	US-08-182-067-2	US-08-039-198B-12	US-08-470-139-26	US-08-836-561-88	US-08-621-751A-6	US-08-933-983-7	US-08-436-717-29	US-08-137-117D-29	US-08-838-692-4	US-08-579-940-2	US-08-157-101A-5	US-08-649-100-17	US-08-436-717-37
Sequence 80, Appl	Sequence 17, Appl	Sequence 8, Appli	Sequence 33, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 12, Appl	Sequence 26, Appl		Sequence 6, Appli	Sequence 7, Appli	Sequence 29, Appl	Sequence 29, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 17, Appl	Sequence 37, Appl

ALIGNMENTS

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; TOPOLOGY: 1i
; MOLECULE TYPE:
US-08-561-521-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                  TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
APPLICATION NUMBER: US/08/
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION UNMBER: 30,22
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
ADDRESSEE: Townsend Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: One ....
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94105
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                               amino acid
                                          linear
                  protein
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ER: 15270-14
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Query Match Best Local Similarity Matches 126; Conserv

Conservative

0;

Mismatches

100.0%;

Score 680; DB 2; Pred. No. 1.3e-59;

Length 126;

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Gaps

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                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
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NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT Saldanha, Jose APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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                     61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                               LENGTH:
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                                                                                                                                                                                      Conservative
                                                                                                                                                                                                    100.0%; Score 680; DB 2; Length 126; 100.0%; Pred. No. 1.3e-59;
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                                                                                                                                                                                   Mismatches
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    PCT-US95-01219-15
; Sequence 15, Application PC/TUS9501219
; GENERAL INFORMATION:
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TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/186
ETILING DATE: 25-JAN-1994
ATTORNEY_AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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APPLICANT:
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APPLICATION NUMBER: PC:
FILING DATE: 25-JAN-19
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                                                                                                                                         121 TKLEIK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                   61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
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ZIP: 94105
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STATE: California
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Jones, S. Tarran
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Leger, Olivier J.
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; MOLECULE TYPE: protein
PCT-US95-01219-15
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                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                         Sequence 4, Application US/08339582
Patent No. 5558852
GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOSYMS-DOS
COMPRATING SYSTEM: PC-DOSYMS-DOS
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CITY: San Francisco
STATE: California
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                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D.
                                                                                                                      APPLICANT: Bigner, Darell D.
APPLICANT: Zalutsky, Michael R.
APPLICANT: Carrel, Stefan
TITLE OF INVENTION: METHOD OF TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
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CORRESPONDENCE ADDRESS:
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          STREET: P.U. CHARLOTTE
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No. 5558852th Carolina
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                                             P.O. Drawer 34009
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Saldanha, Jose
Jones, S. Tarran
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US-08-561-521-5; Sequence 5, A
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Best Local Similarity
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APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 541
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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APPLICATION NUMBER: US 08
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                   STREET: One Market :
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 128 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GKGPRLLMHYTSTLQPGIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLLTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                   ZIP:
                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRPSIQFLGLLLFWLHGAHCDIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118;
                                                                                                                                   94105
                                                                                                                                                                                                                                                                                                                                                                                                                               5840299
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                                                                                                                                                                       California
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                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.2%;
93.7%;
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US/08/561,521
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Pred. No. 4.2e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                       Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.25
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PRIOR APPLICATION DATA:

FILING DATE: CLASSIFICATION:

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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1527
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 5:
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NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15:
TELECOMMUNICATION INFORMATION:
                 TELEFAX: 415-543-5043
                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1:
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                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application PC/TUS9501219
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100.0%; Pred. No. 7.6e-49;
                                                                                                                                                            US 08/186,269
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                                                                        15270-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
                                                                              TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
                                            SEQUENCE CHARACTERISTICS LENGTH: 107 amino acid
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07

FILING DAMPS
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 03-JUL-19
TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercur
                                                                                                                                                                                                  FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 14-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
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                                                                                                                                                 REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                     Carter, Charles
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                                            107 amino acids
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90 South 7th Street, 3100 No. 5972656west Ctr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                linear
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100.0%; Pred. No. 7.6e-49;
                                                                                                                                                                                                                                     US 07/324,392
                                                                                                                                                                                                                                                                                       US 07/493,299
                                                                                                                                                                                                                                                                                                                                       US 07/990,542
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                                                                                                                                                                 35,093
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                                                                                                                                                                     US-08-561-521-7
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                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
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                                                                                                                                                                                     MOLECULE TYPE:
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Local Similarity 91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                           21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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                                                                                                        Local
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                                                                                                                                                                                                                                               CENGTH:
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                              DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98;
                                                                                                      Similarity
                                                                                                                                                                                                                                amino acid
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Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                               106 amino acids
                                                                                                                                                                                                                                                                                               415-543-5043
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                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                   protein
                                                                                                                                                                                                                single
                                                                                                     74.7%;
88.7%;
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                                                                                        Score 508; DB 2; Length 106; Pred. No. 7e-43; 6; Mismatches 6; Indels
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                                                                  Sequence 16, Application US/08235838 Patent No. 5571894 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier APPLICANT: Saldanha, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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 APPLICANT:
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                                                                                                                                                                                                                                                                                       21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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                                                                                                                                                                                                                                                                      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                         94;
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                  Wels, Winfried S.
Hynes, Nancy E.
Harwerth, Ina-Maria
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Saldanha, Jose
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Groner, Bernd
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88.7%;
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Pred. No. 7e-43;
                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 106;
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TITLE OF INVENTION: Recombinate National Receptor TITLE OF INVENTION: Growth Factor Receptor National Of SEQUENCES: 16

Recombinant Antibodies Specific for a

Zwickl, Markus Hardman,

No.

5571894man

APPLICANT:

CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation

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                                                                                                                                                                                                                                                                                                                              Patent No. 5571894
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: GB 91-810079.3 FILING DATE: 05-FEB-1991 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIKG SYSTEM: PC-POS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (908)522 6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 31-JAN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 GGGSDIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 GAQCDIQMTQSPSSLSASLGGKYTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                  CITY:
                                                                                                                                STREET:
                                                                                 COUNTRY:
                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
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ZIP: 07901-6940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
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                                                                   10532
                                                                                                               Hawthorne
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                                                                                                   New York
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                                                                                                                              7 Skyline Drive
                                                                                 USA
                                                                                                                                                                                                                                              Hardman, No. 5571894man
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                CIBA-GEIGY Corporation
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Pred. No. 5.8e-42;
5; Mismatches 10
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; MOLECULE TYPE: protein US-08-235-838-16

TOPOLOGY:

amino acid

linear

TELERAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids

REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614

4-18518/A/CIP/CONT

NAME: Elmer, James Scott REGISTRATION NUMBER: 36,

APPLICATION NUMBER: US 07/828,832 FILING DATE: 31-JAN-1992 PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

FILING DATE:

TBA 435

APPLICATION NUMBER: US/08/235,838

CLASSIFICATION:

APPLICATION NUMBER: GB 9
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:

GB 91-810079.3

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

10532

CITY: Hawthorne

New York

USA

STREET:

7 Skyline Drive

В QΥ 뭉 US-08-465-473B-16 Sequence 16, Application US/08465473B Patent No. 5939531 Matches Best Local Similarity Query Match GENERAL INFORMATION: APPLICANT: Groner, Bernd
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies
TITLE OF INVENTION: Growth Factor Receptor
"""" Growth Factor Receptor NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina Maria
APPLICANT: Groner, Bernd 224 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273 164 GGGSDIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 223 77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126 17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76 STREET: 564 Morris Avenue 74.7%; ilarity 86.4%; Conservative Recombinant Antibodies Specific 5 Score 508; DB 1; Length 637; Pred. No. 5.8e-42; Mismatches 10; Indels 0, Gaps 0;

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-235-838-11
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Matches
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                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
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                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Hynes, Nan
APPLICANT: Harwerth,
APPLICANT: Groner, B
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Recombinant Antibodies TITLE OF INVENTION: Growth Factor Receptor NUMBER OF SEQUENCES: 34
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NAME: Elmer, James Scott
                                                                                                                                                                                                                                           STREET: Summit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9
FILING DATE: 05-FEB-1991
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APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 0' FILING DATE: 31-JAN-1992
                                                                                                                                                                                                          ZIP: 07901-6940
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REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                                                            564 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 amino acids
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86.2%;
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                US 07/828,832
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                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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TELEFAX: (4
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Boque, Llu
APPLICANT: Wlodawer,
TITLE OF INVENTION: R
NUMBER OF SEQUENCES:
                                         REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
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FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
REGISTRATION NUMBER: 22,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
GB 91-810079.3
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    TELEPHONE: (415)
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                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
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                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
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mes 94; Conserv
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Boque, Lluis
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IVENTION: Recombinant Ribonuclease Proteins
RECOUENCES: 64
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ER: 4-18518/A/CIP/CONT2
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Pred. No. 5.7e-42;
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match
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61.2	61.5	61.7	61.7	62.1	62.6	62.6	62.7	62.9	63.0	63.3	63.5	63.8	63.8	63.9	64.0
85	127	124	122	124	128	125	125	129	125	127	117	234	126	141	127
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F36025	A23986	S03521	S40314	S40348	KVMST1	S40349	S40350	S52792	S40316	PH1224	S43528	S14237	A34904	A49134	S11240
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ALIGNMENTS

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A;Cross references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189 C;Superfamily: immunoglobulin v region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                      R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene A;Reference number: A33936; MUID:89282831
A;Accession: C33936
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                 If kappa chain V region (VM113) - mouse (fragment)
C;Specles: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-106 <MEE>
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A; Residues: 1-104 <STA>
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J. Exp. Med. 174, 613-624, 1991
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
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F;16-90/Domain: immunoglobulin homology <IMM>
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Best Local :
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Similarity 95.2%;
          Conservative
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                      77.18;
91.58;
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          5
                      Score 524; DB 2;
Pred. No. 1.6e-38;
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        Mismatches
                                         Length 106;
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A; Residues: 1-103 <ST2>
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A; Residues: 1-103 <STA>
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A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
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A; Accession: S52789
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A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                      A;Cross-references: EMBL:X59187; NID:g52318; PIDN:CAA41897.1; PID:g1334064 A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sea, A;Accession: $26331
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A;Accession: S26332
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C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332; S26331
R;Stark, S.E.; Caton, A.J.
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J. Exp. Med. 174, 613-624, 1991
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A;Description: Light chain V region gene usage restriction and peculiarities in myelo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
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Pred. No. 1.5e-35;
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R.Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444
A;Accession: PH1064
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1064
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                                                                                                                                                                                                                                                                                                                                             R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989

A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325
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A; Residues: 1-94 <LAW>
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87.4%;
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93.8%;
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Pred. No. 1.9e-35;
                                                                                                       Score 476; DB 2;
Pred. No. 1.9e-34;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-23/Region: framework 1
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A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PL0231; MUID:90111618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.2.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990 A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: pL0231; MUID:90111618 A;Accession: PL0272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain V region (anti-DNA, 6B8VK) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000 C;Accession: PL0272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQ
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F;98-107/Region: framework 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-107 <SHL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: PL0270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: PL0270
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C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-107 <SHL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-23/Region: framework 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;35-49/Region:
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                                                                                                          F;57-88/Region: F;89-97/Region: F;98-107/Region:
                                                                                                                                                                                                   F;35-49/Region:
                                                                                                                                                                                                                             F;24-34/Region: complementarity-determining i
                                                                                                                                                                                                                                                   F; 16-90/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                   Query Match
Best Local :
                                                                                                                                                                                  50-56/Region:
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL 114
                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
91;
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                                                                                                                                  complementarity-determining
                                                                                                                                                               framework 3
                                                                                                                                                                                  complementarity-determining
                                                                                                                                                                                                                                                   immunoglobulin homology <IMM>
                                                                                                                                                                                                     framework 2
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                                                                                                                 framework 4
Conservative
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                     68.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 471.5; DB 2; Pred. No. 5.4e-34; 5; Mismatches 9;
  5; Mismatches
                        Score 465.5; DB 2
Pred. No. 1.8e-33;
                                             DB 2;
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                                                Length 107;
    Indels
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A;Reference number: PLO231; MUID:90111618
A;Accession: PLO271
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;35-49/Region: framework 2
                                                                          স্স্স্স
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A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0271
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F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;89-107/Region: framework 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0269
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A; Residues: 1-107 <SHL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Reference number: pL0231; MUID:90111618 A;Accession: PL0269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;16-90/Domain: immunoglobulin homology <IMM>
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                                                                     89-97/Region: 0
  Query Match
                                                                                                                 57-88/Region:
                                                                                                                                        50-56/Region:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 DIOMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
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                                                                                      complementarity-determining
                                                                                                                      framework 3
                                                                                                                                     complementarity-determining 2
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68.3%;
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Score 464.5;
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Pred. No. 2.2e-33;
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DB

2;

Length 107;

Indels

1;

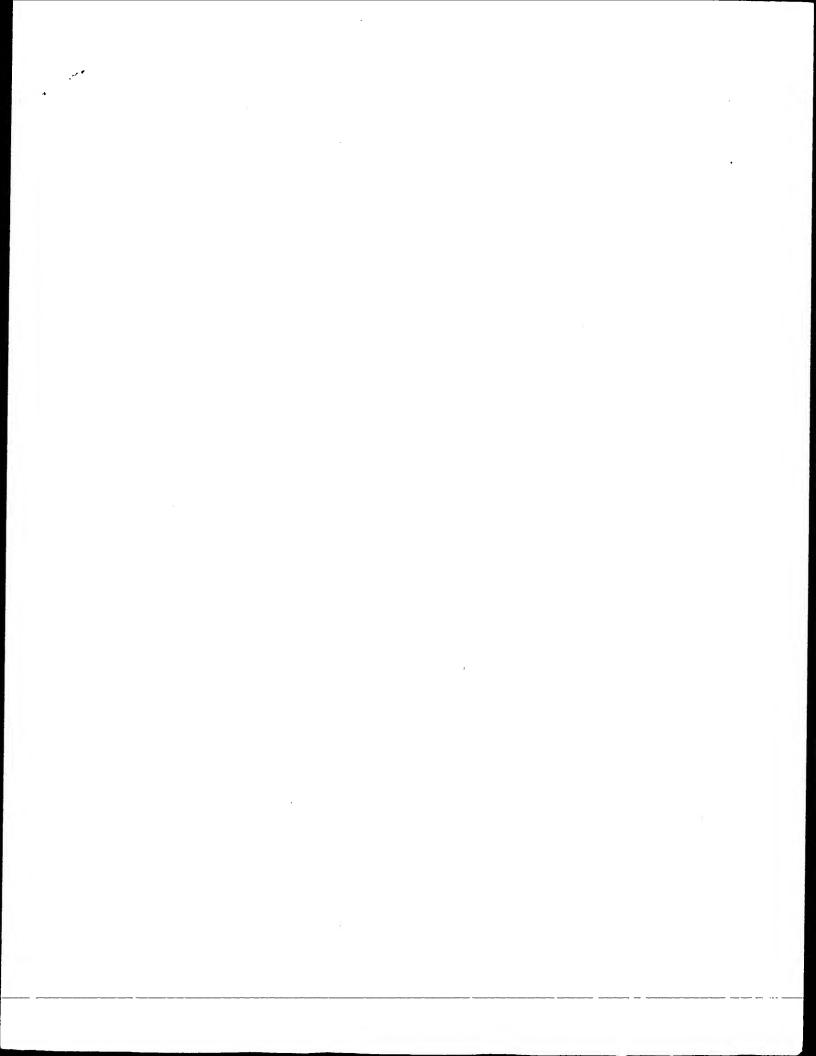
Gaps

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C;Accession: $40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes
A;Reference number: $40312; MUID:94080891
                                                                                                   A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                          Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40334
                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-132 <KLE>
                                                                                                                                                                                                                       A:Status: preliminary; translation not shown
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C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;33-107/Domain: immunoglobulin homology <IMM>
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C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: $40567
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-127 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translation not shown
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        Matches
                         Query Match
Best Local Similarity
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Best Local
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Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 IK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 IK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 LLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYNTPWTFGQGTKVE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 LLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 DIOMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
65.5%; Score 445.5;
64.6%; Pred. No. 1.1;
tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%; Score 453.5; DB 2 68.9%; Pred. No. 2.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
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ches 11;
                       .1e-31
                                      DB 2;
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                                                                                                                                                                                                                                                                                      and their hypermutation.
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C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $40365
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: $40312; MUID:94080891
A;Recession: $40365
A;Status: preliminary; translation not shown
A;Molacule type: mRNA
A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:X72475; NID:9441418; PIDN:CAA51143.1; PID:9441419
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>
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62 GKAPKLLIYVASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFASYYCQQFNSYPFTFGG 121
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COMPLEMENTARITY-DETERMINING 1.
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COMPLEMENTARITY-DETERMINING 2.

SIGNAL CHAIN DOMAIN

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Immunoglobulin

V region;

Signal.

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1 MRPSIOFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAMYQHKP 60

Query Match Best Local Similarity

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re are no restrictions on its as its content is in no way usage by and for commercial http://www.isb-sib.ch/announce/	H.G.; light chain type from two human ated."; 4). It is produced through a collaboration	Euteleostomi; Homo.		P01604 homo sapien P04946 mus musculu P04207 homo sapien P18136 homo sapien P01641 mus musculu P01599 homo sapien P01658 mus musculu P01653 mus musculu P18135 homo sapien P01661 mus musculu P01650 mus musculu P01661 mus musculu P01661 mus musculu P01669 mus musculu P01650 mus musculu

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InterPro; IPR003596; Ig_v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
                                                                                 MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTISCKASQDINSYLTWFQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRVPAQLLGLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKP 62
                                                                                                                                                                                                                                                                                                                                                                                                      SM00406;
                                                                                                                                              Conservative
                                                                                                                                                                                                                     ΑA;
                                                                                                                                                                                                                                                                                                                                                                                      V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                        IGV;
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                                                                                                                                                         62.6%;
                                                                                                                                                                                                                   14385 MW;
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                                                                                                                                              18;
                                                                                                                                                       Score 425.5; DB 1
Pred. No. 2.2e-36;
                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                                                                                                                                                                                                                        FRAMEWORK
                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                                                                                                                                                                  FRAMEWORK
                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                             IG KAPPA CHAIN V-V REGION T1. FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                AFA5563D31BB7E05 CRC64;
                                                                                                                                             Mismatches
                                                                                                                                                                                                                                              SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                      DB 1;
                                                                                                                                          29;
                                                                                                                                           Indels
                                                                                                                                                                      Length 128;
                                                                                                                                          1,
                                                                                                                                       Gaps
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RESULT 4
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVIX_HUMAN STANDARD; PRT; 129 AF PO4432; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update: 15-JUL-1999 (Rel. 38, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A01884; K1HUDI. HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related."; Nucleic Acids Res. 12:6995-7006(1984).
123 GTKVDNK 129
                                                              120 GTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-85014148; Pubmed=6091049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).

Finkarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klobeck H.G., Combriato G., Zachau H.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                        63 GKAPTLLIYAVSNLQVGVPSRFSGSGSGAEFTLTISSLQPEDFATYYCQQNYNFSFTFGG 122
                                                                                                                                                                           61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    w
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                                                                                                                                                                                                                                                                         MRVPAQLLGLLLLWLRRVRCDIQMTQSPSSLSASVGDRVTITCRAGHNITNFLSWYQQKP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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(Rel. 05, Last sequence update)
(Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127
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                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 412.5;
Pred. No. 4.
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BY SIMILARI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAF076BC7E5574C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Best Local
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P01602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION HK102 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Human immunoglobulin variable region genes -- DNA sequences of two V kappa genes and a pseudogene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMARR; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J00245; AAA59087.1; -.
EMBL; Z00001; CAA77292.1; -.
PIR; A01882; K1HU12.
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bentley D.L., Rabbitts T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-81098966; PubMed-6779204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                     MOUSE
     NCBI_TaxID=10090;
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                          Mus musculus (Mouse)
                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                         61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN 113
                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRPSIQELGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
                                                                                               KAPPA CHAIN V-V REGION L6 PRECURSOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288:730-733(1980)
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                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12768 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.1%;
63.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 402; DB 1;
Pred. No. 4.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG KAPPA CHAIN V-I REGION HK102. FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                115
                                                                                                                            update)
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"Differences between germ-line and rearranged immunoglobulin V kappa coding sequences suggest a localized mutation mechanism.";
Nature 291:668-670(1981).
PIR; A01921; KYMSL6.
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SEQUENCE FROM N.A.
MEDLINE-81220975; PubMed-6264318;
Pech M., Hochtl J., Schnell H., Z
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InterPro; IPR003596; Ig_v.
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Eukaryota; Metazoa; (
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1996 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION AU.
                                                                                                          Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E., Schwager P., Steigemann W., Schramm H.J., The structure determination of the variable portion of the
                                                                                                                                                                                                      immunoglobulin L-chain of the kappa-type, protein Au).";
                                                      Bence-Jones protein Au.";
Biophys. Struct. Mech. 1:139-146(1975).
-i- MISCELLANEOUS: THE STRUCTURE OF THE V REGION
MOLECULAR REPLACEMENT METHODS USING THE KNOWN
                                                                                                                                                  X-RAY CRYSTALLOGRAPHY.
MEDLINE=77022433; PubMed=1234024;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           REGION OF THE KAPPA CHAIN REI.
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                         Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972)
                                                                                                                                                                                                                         The of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
                                                                                                                                                                                                                                                  WEDLINE=72189444; PubMed=5028201; Schiechl H., Hilschmann N.;
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 A01862; K1HUAU
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Pred. No. 7.4e-34
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PDB; 1REI; 17-FEB-84.
InterPro; IPR003006; Ig_w.
InterPro; IPR003596; Ig_v.
IMMUNO9106; IGv; 1.
IMMUNO9106ulin V region; Bence-Jones protein; 3D-structure.
DOMAIN 23 FRAMEWORK 1.
DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                    EPP O. Lattman E.E., Schiffer M., Huber R., Palm W.;
"The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";
Biochemistry 14:4943-4952(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). MEDLINE-76039968; PubMed=1182131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kappa-type L-chain, subgroup I (Bence-Jones protein Rei.); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     three-dimensional structure of antibodies, in particular their
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                                                                                                                                             KVIP_HUMAN STANDARD; PRT; 108 AA P01608; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) IG KAPPA CHAIN V-I REGION ROY.
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         -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN
                                     Gamma globulins: structure and function, pp.57-74, Academic Press New York (1969).
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                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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                         -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                           REVISIONS TO 39 AND 41.
                                                                                        Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
                                                                                                      "Chemical structure of 2 kappa-type Bence Jones proteins
                                                                                                                    Hilschmann
                                                                                                                           MEDLINE=68362076; PubMed=5595110;
                                                                                                                                     SEQUENCE
                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                  NCBI_TaxID=9606;
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71.7%;
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Pred. No. 2e-33;
13; Mismatches
                                                                                                                                                       Catarrhini; Hominidae; Homo
                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
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COMPLEMENTARITY-DETERMINING
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                                                          Langer B., Ponstingl H.,
S.;
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P80362;
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DOMAIN 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M., Solomon A., Stevens F.J., Schiffer M., "Comparison of crystal structures of two homologous proteins: structural origin of altered domain interactions in immunoglobulin light-chain dimers.";
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). MEDLINE-95086080; PubMed-7993911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                    SEQUENCE OF 1-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 33:14848-14857(1994).
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                                                                                                                                                                                                                                                                                                                                                                             Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-81267384; PubMed-6167731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                            DOMAIN
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SMART; SM00406; IGv; 1.
Immunoglobulin V regior
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COMPLEMENTARITY-DETERMINING 3.
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COMPLEMENTARITY-DETERMINING
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    FRAMEWORK 3. COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
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NON_TER
SEQUENCE
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                         PIR; A01861; K1HUAG. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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SMART; SM00406; IG;
                                                                                                                                                                                                                                                                                                          MEDLINE-69234734; PubMed=4893682;
                                                                                                                                                                                                                                                                                                                    SEQUENCE
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InterPro; IPR003596; Ig_v.
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                               61
               81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
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108 AA;
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IGv; 1.
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67.3%;
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69.2%;
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                                                                            Score 380.5;
Pred. No. 6.
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COMPLEMENTARITY-DETERMINING
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Best Local :
                                                                                                                       _MOUSE STANDARD; PRT; 130 AA. PO1639; P01640;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-V REGION MOPC 41 PRECURSOR.
SEQUENCE FROM N.A.

MEDLINE-79221900; PubMed-111146;

Seidman J.G., Max E.E., Leder P.;

"A kappa:jmmunoglobulin gene is formed by site-specific recombination
                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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DOMAIN
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-I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN TOW Grammer.
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P01605;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capra J.D., Klap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete amino acid sequence of the variable domains of IgM anti-gamma_globulins (Lay/Pom) with shared idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=77038198; PubMed=824717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION LAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specificities."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO sapiens (Human).
                                                                                                                                                                                                                                                    61 RESCSGSGTDFTETISSLQPEDIATYYCQQYNN-WPPTEGQGTKVEVK 107
                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                21 DIOMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                            \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                          RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                    DIQMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01607; 1REI
                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klapper D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    108
11834 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
49
56
88
97
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
                                                                                                                                                                                                                                                                                                                                                                       65.7%;
                                                                                                                                                                                                                                                                                                                                                                                   55.8%;
                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                   Score 379.5; DB 1
Pred. No. 8.2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK
BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                    739993A95431434A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AA.
                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                               Length 108;
                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                        KV4B_HUMAN
                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                          P06313;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG KAPPA CHAIN V-IV REGION JI PRECURSOR.
                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MEDLINE=86041853; PubMed=2997712;
           SEQUENCE FROM N.A.
                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
VARIANT
                                                                                                                                           KV4B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
CHAIN
                                                                                                                                                                                                      123 GTKLEIK 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 155:465-467(1967).

-!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burstein Y., Schechter I.; "Amino acid seguence of the NH2-terminal extra piece segments of the Precursors of mouse immunoglobulin lambdal-type and kappa-type light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin V region; Signal; Bence-Jones protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01922; KVMSM4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kappa chains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=67056897; PubMed=4162931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 23-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-33.
MEDLINE=77148916; PubMed=403522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    without further somatic mutation.";
Nature 280:370-375(1979).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
                                                                                                                                                                                                                                              63 DGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ray W.R., Dreyer W.J., Hood L.;
Mechanism of antibody synthesis: size differences between mouse
                                                                                                                                                                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                                                1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKYTITCKTSQDINKYMAWYQHKP 60
                                                                                                                                                                                                                                                          GTKLEIK 126
                                                                                                                                                                                                                                                                                           MRAPAQIFGFLLLLFQGTRCDIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEP
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      130 AA;
                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                           STANDARD;
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59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                       14311
                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                     Score 378.5; DB 1; Pred. No. 1.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
MISSING (IN 25% OF THE MOLECULES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAMEWORK 3
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                                                                                                                                                                                                                                                                                                                                                                                                   5EFE0FE71D5F1BEC CRC64;
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                                                                                           update)
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                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                               Length 130;
                                                                                                                                                                                                                                                                                                                                           Indels
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RY11_HI KNV11_HI KNV1
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                      KV1I_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single germline gene.";
Nucleic Acids Res. 13:6515-6529(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zachau H.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klobeck H.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Subgroup IV of human immunoglobulin K light chains is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin V region;
kappa genes and a pseudogene.";
Nature 288:730-733(1980).
[2]
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION HK101 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                        Bentley D.L., Rabbitts T.H.;
                                                                                                              SEQUENCE FROM N.A. MEDLINE=81098966; PubMed=6779204;
                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                     P01601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
                                                                'Human immunoglobulin variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 FLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDI-----NK-YMAWYQHKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TKVEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FISLLL-WISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pF00047; ig; 1.
; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z00022; CAA77317.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14632 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 378.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK 2.

COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK 3
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                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5FB3953066744AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAPPA CHAIN V-IV REGION JI
                                                                                                                                                                                                                                                                                                                                                                                                  117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                          sequences
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"Evolution of immunoglobulin V genes: evidence indicating Evolution of immunoglobulin V genes: evidence indicating the mention of immunoglobulin V genes: evidence indicating the mention of immunoglobulin V genes: evidence indicating the mention of the mentio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=83129397; PubMed=6402305;
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SMART; SM00406; IGv;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-V REGION MOPC 173.
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                                       "Determination of the primary structure of immunoglobulin. Amino-acid sequence of the Eur. J. Biochem. 59:525-537(1975).
                                                                                                                                                   MEDLINE=76091934; PubMed=812696; Schiff C., Fougereau M.;
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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SUMMARIES

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114	97	107 101	106	108	109	109	238	109	298	108	107	107	108	214	108	Length DB
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Q9JL74 Q9UL80	Q9JL76	Q9ERZ9	Q9U410	Q9UL83	Q9UL86	Q9UL85	Q99M37	Q9UL78	Q9QYF0	Q9UL79	Q9UL81	Q9JL84	Q9UL70	Q9R1A5	Q9UL77	ID
mus homo	Q9j176 mus musculu Q9j180 mus musculu		Q9u410 schistosoma	Q9ul83 homo sapien	Q9u186 homo sapien	Q9u185 homo sapien	Q99m37 mus musculu	Q9u178 homo sapien	Q9qyf0 mus musculu	Q9u179 homo sapien	Q9u181 homo sapien	Q9j184 mus musculu	Q9u170 homo sapien	Q9rla5 mus musculu	Q9u177 homo sapien	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	
110	110.5	110.5	111.5	113.5	115	115	115.5	116	117	117	118.5	119	119	124	129	140	140.5	150	185	188.5	193.5	204.5	209	252.5	262	
16.2	16.2	16.2	16.4	16.7	16.9	16.9	17.0	17.1	17.2	17.2	17.4	17.5	17.5	18.2	19.0	20.6	20.7	22.1	27.2	27.7	28.5	30.1	30.7	37.1	38.5	
123	473	372	361	334	509	487	503	418	513	509	342	509	509	169	100	135	93	337	109	235	130	107	107	109	104	
11	11	4	4	13	11	11	4	11	11	11	13	11	11	4	σ	4	4	13	11	11	4	4	4	6	11	
Q61243	Q9D8L4	Q9Y4V0	Q9H1U5	Q9IB05	008907	Q99KA4	P78324	070426	P97797	Q9QX57	Q9IB00	P97710	Q9QWI5	Q9Y2N4	077624	Q9H5Z4	Q9UL76	Q9IB02	Q9ET13	Q99M11	Q9NP29	Q9UL82	Q9NSD6	Q9N0W5	Q9JL82	
Q61243 mus musculu	mus	homo	Q9hlu5 homo sapien			Q99ka4 mus musculu	P78324 homo sapien				Q91b00 sphoeroides		09qwi5 rattus norv	Q9y2n4 homo sapten				N	Q9et13 mus musculu	mus	Q9np29 homo sapien	omo	Q9nsd6 homo sapien	_	\sim	

ALIGNMENTS

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Best Local (
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Q9UL77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TYEMBLIE). 13, Created)
01-MAY-2000 (TYEMBLIE1. 13, Last sequence update)
01-JUN-2001 (TYEMBLIE1. 17, Last annotation update)
01-JUN-2001 (TYEMBLIE1. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR003066; Ig_MHC.
Interpro; IPR003596; Ig_v.
pfam; pF00047; ig; 1.
SMART; SM00406; IGv; 1.
NON TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF035037; AAD56273.1; -. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin-reactive autoantibodies in rheumatic carditis and normal
81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLEIK 126
                                                                                                                                                          21 DIOMTOSPSSLSASLGGKYTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                     DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AA; 11738 MW; C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                           57.3%; Score 389.5; DB 4; Length 108; ilarity 68.2%; Pred. No. 5.6e-35; Conservative 13; Mismatches 20; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108
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Best Local
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HSSP; PO1789; 1MCP.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MIG.
InterPro; IPR003596; Ig_W.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 2
SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like; 1.
                                                                                 SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Mu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                01-MAY-2000 (TremBLrel. 13, Created)
01-MAY-2000 (TremBLrel. 13, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                           Clin.
                                                                                                                                                     NCBI_TaxID=9606
                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFV).", Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.
 -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                        fetus."
                                                  "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9R1A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9R1A5;
                                                                                                                                                                                                                                                                                                                                                                                                                 81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIOMTOSPSSLSASLGGKYTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                    RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK 107
                      Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214
                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 380.5; ; Pred. No. 1.2e 14; Mismatches
                                                                                     P.L.,
                                                                                   Kalis N.N., Berney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                     108 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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Q9UL81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; 1g; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF206022; AAF69320.1;
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                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JL84;
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SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                         interPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003596;
                                                                                               61
                                                                                                                        81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                            21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                       1 DIQMTQSTSSLSASLGDRVXXXCSASQGISNXXXWFQQKPDGTVKLLIYYTSSLXSGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                          RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS
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                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                              107
107 AA;
             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                              Conservative
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11648 MW;
                                                                                                                                                                                                                                            54.8%;
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                                                                                                                                                                                                                                          Score 372.5; DB Pred. No. 4e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 378.5; DB 4
Pred. No. 8.9e-34;
            PRT;
                                                                                                                                                                                                                                                                                                         ACF9B1253ACA1E5D CRC64;
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                                                                                                                                                                                                                           Mismatches
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            107
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                                                                                                                                                                                                                                                          DB 11;
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                                                                                                                                                                                                                                                          Length 107;
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Best Local S
Matches 68
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
                                                                                                                                                                                                                                                                            Q9UL79;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98277139; PubMed-9614934;
Tiu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; 1g; 1.
SMART; SM00406; IGv; 1.
NON TER 1
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HSSP; P80362; 1WTL
                                                                                                                                                                            MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
Yin R. Van der Merwe P.L., Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - i - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                              Q9UL79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                retus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                    Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                         Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                        HSSP; P01607;
                          NON_TER
                                                             InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                            -1- SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                             81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                           RESGSGSGTDETLTISGLQAEDFATYYCQQSYSALTFGPGTKVDIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunol. Immunopathol. 87:184-192(1998).
                                                                                                  AF035035; AAD56271.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
108 AA;
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
              108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                         トスピト
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD56269.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11501 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.2%;
                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
 11787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 362; DB 4;
Pred. No. 5.5e-32;
                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             070549FDE0754748 CRC64;
  DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                             AND
                                                                                                                                                                                                                                                                                                                                                               108
                                                                                                                               MAJOR HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                                                            Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 107;
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RESULT
Q9QYF0
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Best Local Similarity
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Best Local
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9QYFO, PRELIMINARY; PRT; 298 AA.
09QYFO;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                               InterPro; IPRO03006; Ig_MC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shinohara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shinohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB036341; BAA88633.1; HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/C;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                      Q9UL78;
                                                                     Q9UL78
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                              method.
                                                                                                                                                                                           169 GGGSDIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLAD
                                                                                                                                        229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 GIPSRESGSGSGRDYSENISNLEPEDIATYYCLQY-DNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIVMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASTLQSGVPS
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                                                                                                                                        GVPSRFSGSGGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69;
                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N., Demura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DEC-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                       298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                  Conservative
                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                       31867 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.0%; Score 346.5; DB 4; 64.5%; Pred. No. 2.7e-30; tive 12; Mismatches 25;
                                                                                                                                                                                                                                                               50.2%; Score 341.5; 57.7%; Pred. No. 3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fukuda H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Mismatches
                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                        PRT;
                                                                                                                                                                                                                                                                                                                       E0F96B8A17004317 CRC64;
                                                                                                                                                                                                                                                     Mismatches
                                                                        109
                                                                                                                                                                                                                                                                 3e-29;
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                                                                                                                                                                                                                                                                              DB 11;
                                                                                                                                                                                                                                                      28; Indels
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                                                                                                                                                                                                                                                       1;
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Best Local :
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HSSP; P0178; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
NON_TER
                                                                                                                                                                                                                         Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:5947).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                 TISSUE=MAMMARY TUMOR;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                      115 WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                      60
                                                                                56
                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108
                                                                                                                            1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDI-----NKYMAW 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 SRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                            YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVP 119
                                                                       YQHKPGKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL- 114
                                                                                                  MKLPVRLL-VLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. Immunol. Immunopathol. 87:184-192(1998).
SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109
                                                                                                                                                                             46.78;
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                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 319; DB 4; Length 109;
Pred. No. 2.7e-27;
17; Mismatches 27; Indels
                                                                                                                                                                            Score 317.5; DB 1
Pred. No. 9.6e-27;
                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5F675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 AA.
                                                                                                                                                                                        DB_11; Length 238;
                                                                                                                                                                 37;
                                                                                                                                                                 Indels
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                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                01-MAY-2000 (TremBLrel. 13, Created)
01-MAY-2000 (TremBLrel. 13, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                Q9UL86;
EMBL; AF035028; AA HSSP; P01789; 1MCP
                                  SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                           "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                Young D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
NON_TER 1 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF035029; AAD56265.1; HSSP; P01607; 1REI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 YTFGSGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                   81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW---TFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DIOMTOSPSSLSASLGGKYTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              1 EIVMTQSPATLSVSPGERATLSCWASQSISSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60
                            DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN.
                                                                                                                                                                                                                                                                                                                                                          AF035028; AAD56264.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
109 AA;
                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11761 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.6%; Score 310; DB 4; Length 109; 56.0%; Pred. No. 2.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Mismatches
                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                         109 AA
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RESULT
Q9U410
ID Q9
AC Q9
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Q9UL83
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Best Local S
Matches 58
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSS; PO1607; 1REI.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interero: IPR003006; I
Interero: IPR003596; I
Pfam; PF00047; 19; 1.
SMART: SM00406; IGv; 1
NON_TER 1
NON_TER 19 109
SEQUENCE 109 AA; 11
  Q9U410;
Q9U410;
Q1-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TremBLrel. 13, Created)
01-MAY-2000 (TremBLrel. 13, Last sequence update)
01-UN-2001 (TremBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wu X., Liu B., Van der Merwe P.L.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9UL83;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRFSGSGSGRDYSFNISNLEPEDIATYYCLOY-DNLWTFGGGTKLEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRATGIPA 60
                                                                                                                                                                                               RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
                                                                                                                                                        RFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNN-WPFTFGPGTKVDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunol. Immunopathol. 87:184-192(1998)
IMILARITY: TO IMMUNOGLOBULIN AND MAJOR H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF035031;
                                                                                                                                                                                                                                                                                                                                     58;
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IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                             108 AA;
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                                                                                                                                                                                                                                                                                                                                     Conservative
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  (TrEMBLrel.
                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD56267.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11928 MW;
                                                                                                                                                                                                                                                                                                                                                        44.98; 53.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                             11834 MW;
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54.6%;
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Pred.
                                                                                                                                                                                                                                                                                                                                 Score 305.5; DB Pred. No. 8e-26; 1; Mismatches
      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                                                                                                                                               DB 4;
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Best Local
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SEQUENCE
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01-JUN-2001 (TYEMBLIEL 17, Last annotation update)
MONCCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGMENT),
Schistcosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea: Schistosomatid
                                                                                                                                                                                                                                                                                                                                   Chen P., "Cloning genes of J. Cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.; "Amplification, cloning and sequence analysis of the light chain variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal anti-idiotypic antibody NP30 or variable region gene of monoclonal antibody NP30 or variable region gene of monoclonal antibody NP30 or variable region general antibody 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schistosoma japonicum.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ERZ9
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                                                                        SEQUENCE FROM N.A.

Chen P., Deng J.B., Wang Z.L., Han H., Yao L.F.
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003006;
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                                                                                                                                                                         Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., "Construction and sequencing of the single-chain human TNT-alpha specific monoclonal antibody."; Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9ERZ9;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 MTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPSRFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 GSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
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                                                   SIMILARITY:
                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSGSGTSYSLTISRMEAEDAATYYCQQWTSYPFTFGSGTKLELK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF207620; AAF19434.1;
AF262753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                              FROM N.A.

Deng J.B., Wang Z.L., Han H., Su C.Z.;

and sequencing of the light chain fragment
an anti-frne-a monoclonal antibody.";

Mol. Immunol. 12:21-26(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 AA;
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  AAG23804.1;
                                                TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11478 MW; F20F544426BAE63E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.0%;
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Pred. No. 4e-25;
4; Mismatches
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                                                        AND
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                                                        MAJOR
                                                                                                 Yao L.B.,
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                                                     BJ databases.
HISTOCOMPATIBILITY
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                                                                                                                                                                                                                                  Su C.Z.;
antibody
                                                                                                      Su C.Z.;
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Schistosomatidae;
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Q9JI78
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Search completed: May
Job time: 638 sec
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches 55
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InterPro; IPR003006; Ig_wHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-A.CA;
Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9JL78

O9JL78;
O9JL78;
O1-OCT-2000 (TrembLrel. 15, Created)
O1-OCT-2000 (TrembLrel. 15, Last sequence update)
O1-JUN-2001 (TrembLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF206028; AAF69326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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                                                                                                                                                                                88 GRDYSFNISNLEPEDIATYYCLQYDNL--WTFGGGTKLEIK 126
                                                                                                                                                                                                                                                         61 GTSYSLTIGTMEAEDVATYYCQQGSSIPRYTFGGGTKLEIK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VPDRFMGSGSGTDFTLTISSVQTEDLADYFCQQHYRTPFTFGSGTKL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 IPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTPGGGTKL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity nes 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 MTQSPSSLSASLGGKVTITCKTSQDI------NKYMAWYQHKPGKRPRLLIHYTSALQPG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 AA; 11784 MW;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10778 MW; 0A7F65E6A7E6F14D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 43.0%; Score 292.5; DB 1
56.4%; Pred. No. 1.9e-24;
tive 16; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.5%; Score 295.5; DB 11; Length 51.4%; Pred. No. 9.7e-25; tive 21; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2B15EEA6604A26C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 101;
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                                                                                                                                                                                                                                                                                                                                                                                        25;
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein -
                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                             Query
Match
  100.0
100.0
86.5
84.9
84.3
83.8
79.8
79.6
79.2
78.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-155-739-4
746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                 : /SIDSB/gcgdata/geneseq/yeneseqp/AA1980.DAT: *
:/SIDSB/gcgdata/geneseq/yeneseqp/AA1981.DAT: *
:/SIDSB/gcgdata/geneseq/yeneseqp/AA1982.DAT: *
:/SIDSB/gcgdata/geneseq/yeneseqp/AA1983.DAT: *
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                                                                                                                                                                                                                                                             Length DB
                                                                    140
123
136
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136
    116
117
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118
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119
119
118
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  AAR81327
AAW22410
AAR81330
AAW04379
AAR11384
AAR76664
AAR41679
AAW21845
AAW21845
AAW63828
AAW63828
                                                                                                                                                                                                                                                                                                                                 SUMMARIES
Murine ONS-21 anti
V heavy chain of r
Heavy chain variab
Human Mab #117-10C
Human VLA-4 reshap
Humanised alpha-4
                                                                                                                                                                                                                                                                Description
                                                                                                                                                                          Mouse VLA-4 antibo
Alpha-4 integrin m
Mouse anti-VLA-4 a
                                                                                                                                 Chimaeric human/mu
Variable gamma hea
```

Transformant CDM/1	AAW63830	19	119 248	67.2	501
	AAR15443	12	240	67.2	501.5
chain '	AAR15437	12	116	7.	501.5
Chimaeric human/mu	AAW04396	17	136	67.3	502
Human/murine chime	AAR76681	16	136	7.	502
VEGF antagonist an	AAB82701	22	136	7.	503
Murine anti-botuli	AAY30123	20	254	7.	504
anti-botul	AAY30121	20	254	7.	504
	AAY30119	20	254	7.	504
	AAY30117	20	254	7.	504
	AAW29750	18	139	7.	505.5
MAD CT-M-01 heavy	AAY56873	21	138	7.	505.5
	AAR39566	14	120	8	508
	AAR15439	12	126	8	509.5
Murine anti-VLA-4	AAB73462	22	120	8	511
Anti VLA-4 antibod	AAY01033	20	120	ω.	511
ਧ	AAY23984	20	120	8	511
Ab HE	AAR58749	15	120	8	511
	AAR39817	14	120	68.5	511
	AAW96744	20	121	8	513
Heavy chain variab	AAW96741	20	121	9	516
Anti-EGFR antibody	AAR79889	16	120	69.2	516.5
VLA4	AAR59942	15	143	9	517
chai	AAR60527	15	113	9	518.5
chain	AAW44121	19	120	9.	521.5
Heavy chain variab	AAR30767	14	120	9	521.5
	AAY53590	21	122	.0	524.5
S	AAW37738	19	437	71.8	535.5
Humanised alpha-4	AAW22413	18	123	2	1.1
A heavy chain vari	AAB07969	21	135	2	539.5
Humanized VLA-4 an	AAR81323	16	123		ū
HNK-20 variable he	959	17	w	76.5	
Amino acid sequenc	AAB07967	21	135	77.3	76.

ALIGNMENTS

AAR81327 standard; Protein; 140 AA

RESULT AAR81327

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XX PN W09519790-A1.	FT	FT Region	FT	FT Region	FT	FT Region	FT	FT Region	FT	FT Region	FT	FT Region		FT Region		FT Peptide		XX	OS Mus musculus			DE Mouse VLA-4 a	23-MAR-1996	AC AMNOTORY,
	/note= "framework region 4"	132140	/note= "complementarity determining region 3"	118131	/note= "framework region 3"	86117	/note= "complementarity determining region	6985	/note= "framework region 2"		/note= "complementarity determining region 1"	5054	/note= "framework region 1"	2049	/note= "signal peptide"	119	Location/Qualifiers			neering.	Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeuti	Mouse VLA-4 antibody 21.6 light heavy variable region.	(first entry)	

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RESULT
AAW22410
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                  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents the mouse antibody 21.6 heavy chain variable credity of directed against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 VH and VL (see AAQ9989) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ9989-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized heavy chain, amino acids H27, L28, H29, H30, H44 nd H71 in the human HC VR framework are replaced by the amino acid present in the equivalent position of the mouse classification of a leukocyte to an endothelial cell and considered into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and considered in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4. for affinity nurrification or for generating the constant of the mouse can also be used for detecting VLA-4. for affinity nurrification or for generating the constant of the mouse can also be used for detecting VLA-4. for affinity nurrification or for generating the constant of the mouse can be used to the constant of the mouse can also be used for detecting VLA-4. for affinity nurrification or for generating the constant of the mouse can be used to the constant of the mouse constant of the mouse constant of the mouse constant of the constant of the mouse constant of the mouse constant of the mouse constant of the constant of the constant of the mouse constant of the constant
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                                                                               Alpha-4 integrin mouse MAb 21.6 VH region.
                                                                                                                                                                              08-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                 AAW22410 standard; Protein; 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        meningitis or encephalitis. The antibodies can also be used detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-idiotype antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ATHE-) ATHENA NEUROSCIENCES INC
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Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 746; DB 16;
Pred. No. 5.9e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating
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This polypeptide comprises the heavy chain variable region (VH) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VH can be incorporated into a human 21/28 CL framework to produce a claimed incorporated into a human 21/28 CL framework to produce a claimed in the manufacture of a medicament for antibody that is used in the manufacture of a medicament for treating a disease selected from asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid archiritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte mediated lung injury. The antibody may also be used in the affinity purification of alpha-4 integrin for use as a vaccine or an immunogen. It is also useful for
        equivalent to that
             for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibodies of the invention have a half-life in the human circulation essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 69-70; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uses of humanised alpha-4 integrin antibody - asthma, atherosclerosis, AIDS, dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-297879/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bendig MM, Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1995;
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acute leukocyte mediated lung injury; therapy.
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55,.68
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of naturally occurring human antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for treatment
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Query Match
Best Local Similarity
Matches 140; Conserv

Conservative

100.0%; Score 746; DB 18; 100.0%; Pred. No. 5.9e-60; tive 0; Mismatches 0;

Length 140; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
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                                                                                                                                                                                                   25-JAN-1995;
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                         WPI; 1995-269276/35
                                                                  Bendig MM, Jones TS,
                                                                                                            (ATHE-) ATHENA NEUROSCIENCES INC.
                                                                                                                                                       25-JAN-1994;
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                                                                                                                                                       94US-0186269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "mouse heavy chain variable framewor)
    region 3"
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region 4"
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                                                                  Leger OJ,
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region 2"
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PT New humanised antibodies against VLA-4 - used for inhibiting pri leukocyte adhesion to endothelial cells, partic. for treating PT leukocyte adhesion to endothelial cells, partic. for treating PT inflammatory disease.

XX Disclosure; Page 68; 105pp; English.

XX The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain CC variable region (without signal sequence). Cloned cDNA CDR sequences of mouse 21.6 variable light and variable heavy regions are linked to human constant framework regions of the REI antibody for the light chain and the 2*CL antibody for the heavy chain in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into constant regions. In the humanized light chain, amino acids L45, L49, CC L58 and L69 in the humanized alight chain, amino acids L45, L49, CC L58 and L69 in the equivalent position of the mouse 21.6 Ig light chain. Plasmids encoding the chimeric antibodies are transfected into CC cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.

XX Sequence 123 AA;
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                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                      Heavy; variable region; murine; human; myeloblastoma; chimaera; monoclonal antibody; chimera; single stranded Fv region; low human antigenicity; diagnosis; treatment; cerebral tumour;
                                                                                                                                                                                                 Chimaeric human/murine MAb ONS-M21 variable heavy region
                                                                                                                                                                                                                    04-DEC-1996
                                                                                                                                                                                                                                                              AAW04379 standard; Protein; 136 AA.
         Region
                                                 Region
                                                                      Peptide
                                                                                                                         Synthetic
                                                                                                                                                                                                                                         AAW04379;
                             Region
                                                                                           Peptide
                                                                                                                                             reshaped.
                                                                                                                                                                                                                                                                                                                 121 v 121
                                                                                                                                                                                                                                                                                                                                    140 V 140
                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                           20 EVQLQQSGAELVKPGASVKLSCTÄSGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                        evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 60
                                                                                                                                                                                                                                                                                                                                                                             DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                          121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                    (first entry)
118..125
/label= (
                                                 50..54
                             /label= CDR_1
69..85
                                                                      /label= sig_peptide 20..136
                                                           /label= mat_peptide
                                                                                                   Location/Qualifiers
                    /label= CDR_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.5%; Score 645; DB 16; 100.0%; Pred. No. 6.5e-51;
 CDR_3
                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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RESULT
AAR11384
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   FFH XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the variable heavy region of the Chimaeric human/murine monoclonal antibody (MAB) ONS-M21. The MAB CWas prepd. by combining light and heavy variable region DNA, from a murine anti-human myeloblastoma cell MAB, with human light cand heavy constant region sequences, respectively to produce chimaeric human/murine light and heavy chain DNA mols. A recombinant vector for the expression of the heavy and light chain DNA mols. was prepd., and used to transform a host cell. The host cell was then cultured, and the expression prods. of the heavy and light chain DNA mols. sepd. and connected with a peptide linker to produce a single stranded Fv region. The reshaped Fv region has an agent for the diagnosis and treatment of cerebral tumours, ce.g. myeloblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 125;
 Peptide
                                        Mus musculus
                                                                             MAb T84.66; gamma heavy chain; carcinoembryonic antigen; CEA,
                                                                                                           Variable gamma heavy chain of T84.66 monoclonal antibody.
                                                                                                                                         08-MAY-1991 (first entry)
                                                                                                                                                                                                  AAR11384 standard; Protein; 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reshaped anti-human myeloblastoma cell human antibody - has low human antigenicity, and is therefore useful for diagnosis and treatment of cerebral tumours, e.g. myeloblastoma
                                                                    human adenocarcinoma; mouse-human chimaeric antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 22; 45pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-358509/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-1994;
19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT38600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-1996
                                                                                                                                                                                                                                                                       120 yvn-----qdywgqgtsvtv 134
                                                                                                                                                                                                                                                                                   121 YGNYGYYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHUS ) CHUGAI PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP08169900-A
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                                                                                                                                                                                                                                                                                                                                                                                                             1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93JP-0291078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94JP-0252166.
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Location/Qualifiers 20..38
                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 633; DB 17; Length 136; Pred. No. 8.8e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
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                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
Plasmid pUC-M21-V(H); murine; ONS-M21 antibody; chimeric protein; medulloblastoma; brain tumour; treatment; diagnosis.
                                     Murine ONS-21 antibody variable heavy chain.
                                                            16-JAN-1996 (first entry)
                                                                                          AAR76664;
                                                                                                                AAR76664 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                             The heavy chain variable region of murine MAb 84.66 was cloned and sequenced. It was used to produce mouse V-human C antibodies with high affinity for CEA. Chimaeric murine-human anti-CEA Abs are used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 18; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel anti-CEA antibody - comparable to ATCC Accession No. BH 8747, produced by recombinant DNA, used in diagnosis of tumours
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shively JE, Riggs AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ11098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-073486/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-1990;
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                                                                                                                                                                                                  121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CITY ) CITY OF HOPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                        61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                             gnose human colon adenocarcinomas.
also AAQ10834-Q10848.
                                                                                                                                                                            y--vsdyamaywgqgtsvtv 138
                                                                                                                                                                                                                        eqglewigridpangnskyvpkfqgkatitadtssntaylqltsltsedtavyycapfgy 120
                                                                                                                                                                                                                                                                                                                            123;
                                                                                                                                                                                                                                                                                                                                                                                     140 AA;
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89US-0385102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90WO-US04049
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39..49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "sequenced as peptide fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= tryptic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= tryptic peptide
/note= "sequenced as peptide fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label = complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
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                                                                                                                                                                                                                                                                                                                                    84.38;
87.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "sequenced as peptide fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neumaier M;
                                                                                                                                                                                                                                                                                                                        Score 629; DB 12; Length 140; Pred. No. 2.1e-49; 6; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determining region
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RESULT
AAR41679
ID AAR4
XX AAR4
AC AAR4
XY 24-P
TY 24-P
XX V he
XX V he
XX Infe
KW Anti
XX Synt
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Best Local
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                AAQ94485 is the plasmid pUC-M21-V(H), which encodes AAR76664 the murine antibody ONS-21 variable heavy chain. The plasmid was used in the construction of an expression vector, conty. cDNA encoding a human/murine chimeric antibody, reactive with human medulloblastoma (a brain tumour) cells. The chimeric antibody can be used in the diagnosis and treatment of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reconstituted antibody against human medullo:blastoma contains high proportion of human antibody origin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohtomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9514041-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                           V heavy chain of recombinant anti-feline calcivirus antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 59; 120pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHUS
                                                                                                     AAR41679;
                               infection;
                                        Antibody; feline calcivirus; FCV; neutralise;
                                                                                 24-MAR-1994
                                                                                                                        AAR41679 standard; Protein;
                                                                                                                                                                           120
                                                                                                                                                                                               121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                   61
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                                                                                                                                             7
                                                                                                                                                                                                                                                                   MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1995-200347/26
                                                                                                                                                                                                                 mkcswvmfflmavvtgvnsevqlqqsraelvkpgasvklsctasgfnikdtyihwakqrp 60
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                                                                                                                                                                                                                                                                                                  124;
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                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                     136
                              diagnosis;
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                         -qdywgqgtsvtv 134
                                                                                (first
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20..136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsuchiya M;
                                                                                entry)
                                                                                                                                                                                                                                                                                                           83.8%;
                               treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                         136
                                                                                                                                                                                                                                                                                                 Score 625; DB 16;
Pred. No. 4.6e-49;
2; Mismatches 8;
                                                                                                                         ₿
                              prophylaxis.
                                                                                                                                                                                                                                                                                                  ,,
                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                        AAW21845
                                                                                                                                                                  RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                  The gene fragment encoding the V heavy chain region is used to produce a genetically engineered antibody capable of reacting specifically with feline calcivirus (FCV). The antibody can be to treat, prevent and diagnose FCV infection. It has a broad neutralising spectrum and can be used to neutralise viruses whave acquired immunity to other neutralising antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP561194-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                   Complementarity determining region; CDR; heavy chain; variable region; murine; mouse; human; interleukin 5; receptor; alpha chain; monoclonal antibody; hybridoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1-2; Figure 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-feline calcivirus recombinant antibody - used to treat, prevent and diagnosis infection and is safe but effective in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ48001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-296521/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tokiyoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kimachi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-1992;
                 chronic bronchitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KAGA ) CHEMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1993;
                            assay; diagnosis; allergic respiratory disease;
                                                                               Heavy
                                                                                                                          AAW21845;
                                                                                                                                              AAW21845
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                      19-DEC-1997
                                                                                                                                                                                                  121
                                                                                                                                                                                                             121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                                                                                                      EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                             116;
                                                                                 chain variable
                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                 136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maeda H,
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                               -laywgqgtlvtv
                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SERO THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92JP-0079189
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69..86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Complementary
118..125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                       79.8%;
82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36pp;
                                                                                 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mikami
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                               137
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~-
                                                                                 of KM1486 antibody.
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                                                                                                                                                                                                                                                                                                                            Score 595; DB 14;
Pred. No. 2.3e-46;
8; Mismatches 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishiyama
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The antibody can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tohya
                                                                                                                                                                                                                                                                                                                                                 Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                              Indels
                                                             treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cats
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RESULT
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                                                                                                                                                                                                                                                                               Matches 116;
                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                           murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal antibody (MAb) KM1486. KM1486 is produced by the hybridoma FERM BP-5651, which was prepared by immunising Balb/c mice with hIL-5R alpha, fusing spleen cells obtained from the mice with mouse myeloma P3-U1 cells and screening the resultant hybridomas. The MAb can be used to detect or assay for hIL-5R alpha and cells expressing it on their surface, especially to diagnose allergic respiratory diseases, e.g. chronic bronchitis. It can also be used
28-SEP-1998 (first entry)
                               AAW63828;
                                                     AAW63828 standard; Protein; 138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody against alpha-chain of human interleukin 5 receptor - useful for diagnosis and treatment of respiratory allergic diseases, e.g. chronic bronchitis
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Pages 124-125; 238pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-202249/18.
N-PSDB; AAT73612.
                                                                                                                                                                                                                                                                                                                                                                       to treat such diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the heavy chain variable region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-SEP-1996;
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                                                                                                                                              121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                 9
                                                                                                                                                                                  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                      mkcswvifflmavvtgvnsevqlqqsgaelvkpgasvnlsctasgfnikdtymhwvkqrp 60
                                                                                                                   -gglrlrffdywgqgttltv 135
                                                                                                                                                                      eqglewigridpangntksdpkfqakatiaadtssntaylqlssltsedtavyyct----
                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ~
                                                                                                                                                                                                                                                                                                                                               137
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Takatsu !
                                                                                                                                                                                                                                                                              Conservative
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50..54
/label= complementarity_determining_region_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= sig_peptide
                                                                                                                                                                                                                                                                                        79.6%;
82.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementarity_determining_region_3
                                                                                                                                                                                                                                                                                        Score 593.5; DB 1
Pred. No. 3.2e-46;
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iida A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koike M;
                                                                                                                                                                                                                                                                                                     DB 18; Length 137;
                                                                                                                                                                                                                                                                           13;
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Query Match
Best Local Similarity
Matches 117; Conserv
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21-FEB-1997;
06-JUN-1997;
                                                                                                                                                                                                           gravis, systemic scleroderma, systemic lupus erythematosus, polyleptic cold haemoglobinuria, polymyositis, periarteritis nodosa, multiple sclerosis, Addison's disease, purpura haemorrhagica, Basedow's disease, leukopaenia, Behcet's disease, climacterium praecox, rheumatoid arthritis, rheumatopyra, chronic thyroiditis, Hodgkin's disease, HIV, asthma, atopic dermatitis, allergic nastitis, pollinosis, apitoxin-allergy and septic shock resulting from production or
                                                                                                                                                                                                                                                                                                                                                    Such antibodies can also be used to detect the II-18 receptor protein (labelled with an enzyme or a radioactive or fluorescent substance). The protein is used to treat e.g. graft rejection, pernicious anaemia, atrophic gastritis, insulin-resistant diabetes, Wegener granulomatosis, discoid lupus erythematosis, ulcerative colitis, cold-agglutinin-relating diseases, Goodpasture's syndrome, primary biliary cirrhosis, sympathetic ophthalmitis, hyperthyroidism, juvenile onset type diabetes, Sjogren
                                                                                                                                                                 Sequence
                                                                                                                                                                                           apitoxin allergy and septic shock resulting from producti administration of excessive gamma interferon (IFN-gamma).
                                                                                                                                                                                                                                                                                                                                       syndrome, autoimmune hepatitis, autoimmune haemolytic anaemia, myasthenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy chain variable region which is used in a method involved in neutralising IL-18 or to treat autoimmune diseases or as an immunosuppressant using anti-IL-18 antibodies which can inhibit IL-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the human monoclonal antibody (Mab) #117-10C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New interleukin-18 receptor protein used to inhibit interleukin-18, to treat autoimmune disease and as immunosuppressant - and new monoclonal antibody and hybridoma used to detect interleukin -18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3.3a; Page 22; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-335317/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kunikata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin-18: IL-18; human; treatment; autoimmune disease; Mab; immunosuppressant; inhibitor; receptor protein; detection; heavy monoclonal antibody; Mab; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Mab #117-10C heavy chain variable region protein fragment.
AAV44000.
                                                                                                                                                                 138 AA;
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kurimoto M,
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96JP-0356426.
97JP-0052526.
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20..138
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                                                                                       79.2%;
83.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Torigoe K,
                                                                          4; Mismatches
                                                                                       Score 591; DB 19;
Pred. No. 5.5e-46;
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                                                                                                         Length 138;
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Qy Db

61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120

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Gaps

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60

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В
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                                                             The sequence represents the human reshaped antibody 21.6 heavy chain variable region against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 216 VH (AAQ99892) and VL (AAQ99889) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (AAQ99895-98) and then
subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized heavy chain, amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig H chain. Plasmids encoding the
                                                                                                                                                     Disclosure; Fig 11; 105pp; English.
                                                                                                                                                                                                                                             WPI; 1995-269276/35.
                                                                                                                                                                                                                                                                                                                     25-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanized antibody; leukocyte adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human VLA-4 reshaped antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR81333 standard;
                                                                                                                                                                               inflammatory disease.
                                                                                                                                                                                          New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                            (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-1996
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118..131
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86..11
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55..68
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50..54
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132..1
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20..49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                      "framework region
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                                                                                                                                                                                                                                                                   Leger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "complementarity determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.6 light heavy variable region.
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                                                                                                                                                                                                                                                                      Saldanha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecule;
              present in the equivalent
                                                                                                                                                                                                                                                                    ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLA-4;
                                                                                                                                                                                          for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW22428
ID AAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for
                                                                                                                                                                                                                                                                                                                                                                          asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermattis; psoriasis; myocardial ischaemia;
                                                                                                                                                                                                                                                                                                                   Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised alpha-4 integrin antibody 21.6 VL version
                          Region
                                                              Region
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                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW22428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW22428 standard; Protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    generating anti-idiotype antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                                                                                                                                                                                                                                                                                                                                                   leukocyte mediated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                 synthetic
                                                                                                                                                                                                                                                                                                                                        Mus musculus;
                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                              sapiens;
                                                              /label= CDR2
/note= "21.6
86..117
                                                                                                    /note=
68..85
                                                                                                                                        /note=
55..67
                                                                                                                                                                              /note=
50..55
/note= "21.6 complementarity determining region
                          /note= "21/28'CL framework region
118..131
                                                                                                                                                    /label= CDR1
/note= "21.6
                                                                                                                                                                                                                            /label= Mat_protein
/note= "VH version |
                                                   /label= FR3
                                                                                                                           /label=
                                                                                                                                                                                                     /label= FR1
                                                                                                                                                                                                                                                                  /label= Leader
                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.3%;
77.1%;
                                                                                                               "21/28'CL
                                                                                                                                                                                        "21/28'CL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 584; DB 16; Pred. No. 2.4e-45;
                                                                         complementarity determining
                                                                                                                                                                                                                                                                                                                                                                 injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                       framework region
                                                                                                              framework region
                                                                                                                                                                                                                            Ha (Claim 25)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 142;
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                                                                                                                                                                    AAB07967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide, designated Ha, comprises the heavy chain variable CC region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also CA AW22413). It is composed of complementarity determining regions from CC the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal cantibody 21.6 and a modified human 21/28/CL framework. It can be carperssed in mammalian host cells following PCR amplification and CC mutagenesis of appropriate mouse and human DNA sequences. The numanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used CC to produce a claimed humanised 21.6 VL (see AAW22412) can be used CC to produce a claimed humanised 21.6 VL (see AAW22412) can be used CC manufacture of a medicament for treating asthma, atherosclerosis, CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid carbinostasis, nephritis, atopic dermatitis, proriasis, myocardial CC ischaemia, and acute leukocyte mediated lung injury. The humanised cantibody has a half-life in the human circulation essentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uses of humanised alpha-4 integrin antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-297879/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-1996;
     autoimmune
                   Antibody 1f1; B7 molecule; B7; humanised immunoglobulin;
                                                  Amino, acid sequence of heavy chain variable region of 1F1 antibody
                                                                                      14-NOV-2000
                                                                                                                                                    AAB07967 standard; Protein; 135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equivalent to that of naturally occurring human antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 6; Fig 11; 107pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9718838-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                 121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                  121 ygnygvyamdywgggtlvtv 140
                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                    gqrlewmgridpangytkydpkfqgrvtitadtsastaymelsslrsedtavyycaregy
                                                                                                                                                                                                                                                                                                                EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis, AIDS,
   disease; infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0561521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= FR4
/note= "21/28'CL framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.3%;
77.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 584; DB 18; Pred. No. 2.4e-45;
disease; inflammatory disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dementia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yednock TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                murine antibody IF1. The antibody has a binding specificity to B7 molecules. The antibody is used to construct humanized immunoglobulins, which comprise an antigen binding region of non-human origin and a portion of a human immunoglobulin. The humanized immunoglobulins are useful for treating autoimmune diseases, infectious diseases, inflammatory disorders, systemic lupus erythematosus, diabetes mellitus, insulitis, asthma, arthritis, inflammatory bowel disease, inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient or preventing transplant rejection in a transplant recipient, and treating proliferative disease the teachers, lymphoma and cancer), anaemia (sickle-cell anaemia, the letter of the state of the sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              systemic lupus erythematosus; diabetes mellitus; insulitis; asthma; arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis; multiple sclerosis; transplant rejection; proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents the heavy chain variable region of the murine antibody 1F1. The antibody has a binding specificity to B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aplastic anaemia; myeloid dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Fig 6A; 162pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modulates
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24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-2000; 2000WO-US03303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200047625-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thalassemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEMY ) GENETICS INST INC.
61
                                                                                                                   1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGENIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GS,
EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                        \verb|mkcswvifflmavvtgvnsevhlqqsgaelvrpgalvklsckpsgfnikdyymhwvkqrp|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-524532/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vasquez M,
, Knight A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin having a binding specificity to B7-1 (derived PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune responses and can therefore treat e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and aplastic anaemia), inborn errors of metabolism, immunodeficiency diseases, and mycloid dysplasia syndrome.
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0339596
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50..54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carreno
O'hara
                                                                                                                                                                                                                                                                                 77.3%;
80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ď,
                                                                                                                                                                                                                                          6;
                                                                                                                                                                                                                                                                                 Score 576.5; DB 2
Pred. No. 1.1e-44;
                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celniker AC,
Rup B, Veld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Veldman GM;
                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collins M,
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                   Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region 1"
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                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                         CC AAR95946-R95948 represent sequences for variable regions of an antibody CC produced by the hybridoma cell line HNK-20. This sequence represents CC the sequence for the antibody HNK-20 variable heavy chain. HNK-20 is a CC murine hybridoma cell line, that produces JgA specific for the F CC glycoprotein of respiratory syncytial virus (RSV). The DNA encoding CC these sequences were isolated using primers specific for the F CC untranslated region of the variable region, and for the intron CC downstream of the rearranged J region (see AAT30459-T30545 for primer CC sequences). The DNA encoding these sequences can be inserted into vectors CC containing heterologous (such as human) constant region genes, for the CC containing heterologous (such as human) constant region genes, for the CC are useful in the treatment and diagnosis of infection by RSV, such as CC are useful in the treatment and diagnosis of infection by RSV, such as CC encoding the treatment and diagnosis of infection by RSV, such as CC as a template, variable region genes can be isolated without producing CC Also, by using the genomic DNA, no knowledge of the DNA sequence CC encoding the target variable region is required. Chimeric antibodies CC host being treated, are less likely to cause adverse immune reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR95948
                                                                          Matches 114;
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody; HNK-20; variable heavy chain; hybridoma; murine; IgA; mouse; F glycoprotein; respiratory syncytial virus; RSV; constant region gene; chimeric antibody; isotype-switched antibody; therapy; infection; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Fig 5d;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HNK-20 variable heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR95948 standard; Protein; 137
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              respiratory syncytial virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding variable region of antibody HNK-20 - for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT30458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-286826/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berdoz J, Kraehenbuhl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ORAV-) ORAVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pneumonia; bronchiolitis; animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 f-----faywgqgtpvtv 133
                                                                                           Local Similarity
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75pp; English
                                                                                           76.5%;
81.4%;
                                                                          6;
                                                                                           Score 570.5; DB 1
Pred. No. 3.8e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                          Mismatches
                                                                                                           DB 17;
                                                                          15;
                                                                          Indels
                                                                                                         Length 137;
                                                                          5.
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20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79

Matches 100;

Conservative

11;

Score 544; DB 16; Pred. No. 8.2e-42; .1; Mismatches 10;

Length 123; Indels

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72.98; 82.68;

Local Similarity

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AAR81323
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The sequence encodes the mouse antibody 21.6 heavy chain variable cregion, Ha, directed against leukocyte adhesion molecule VIA-4. Cloned CDNA sequences of mouse 21.6 VL and VH (AAO99889 and AAO99892) regions are linked to human constant regions in the construction of a humanized antibody against VIA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAO9989-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the humanized light chain, amino acids L45, by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for treating inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR81323 standard; Protein; 123
                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 69; 105pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bendig MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09519790-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
Sequence
                               anti-idiotype antibodies.
                                               meningitis or encephalitis. The antibodies can also be used detecting VLA-4, for affinity purification or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disease.
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123
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RESULT 1
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                                                                                                                Humanized
from ATCC
The gresent sequence represents the heavy chain variable region of the humanişed murine antibody IF1. The antibody has a binding specificity to B7 molecules. The antibody is used to construct humanized immunoglobulins, which comprise an antigen binding region of non-human
                                                              Example 10; Fig 7A; 162pp; English.
                                                                                         diseases, infectious diseases
                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      systemic lupus erythematosus; diabetes mellitus; insulitis; asthma; arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis; multiple sclerosis; transplant rejection; proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
                                                                                                                                                                                                    Co MS,
                                                                                                                                                                                                                            (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                    12-FEB-1999;
24-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A heavy chain variable region of humanised 1F1 antibody.
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                                                                                                                                                                                       GS,
                                                                                                                                                    2000-524532/47.
DB; AAA59698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
                                                                                                                                                                                      Vasquez M,
, Knight A,
                                                                                               immunoglobulin having a binding specificity to B7-1 (derived PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules, immune responses and can therefore treat e.g. autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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99US-0339596.
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50..54
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                                                                                                                                                                                                                                                                                                                                                                          /note= "complementarity determining region 1" 118...124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 1..19
                                                                                                                                                                                                                                                                                                                                                             /note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                            'note= "complementarity determining region 1"
                                                                                                                                                                                      Carreno B,
O'hara D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                     "mature protein"
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                                                                                                                                                                                                  Collins M,
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                                                                                                                                                                                                                                                                                                                                                                                             origin and a portion of a human immunoglobulin. The humanized immunoglobulins are useful for treating autoimmune diseases, infectious diseases, inflammatory disorders, systemic lupus erythematosus, diabetes mellitus, insulitis, asthma, arthritis, inflammatory bowel disease, inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient or preventing transplant rejection in a transplant recipient, and treating proliferative disease (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia, thalassemia and aplastic anaemia), inborn errors of metabolism, congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
                                                                                                                                                                                                                                                                                                                                                           Sequence
121 f-----faywgqgtlvtv 133
                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                          1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                              YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                               mkcswvifflmavvtgvnsevqlvqsgaevkkpgasvkvsckpsgfnikdyymhwvrqap 60
                                                                                                                      EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                      105;
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                                                                                                                                                                                        72.3%;
75.0%;
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Pred. No. 2.3
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Job time: Search completed: 246 sec Мау 7, 2002, 12:22:25

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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Copyright (c) 1993 - 2000 Com
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PCT US95-01219-9
US-08-646-2658-29
US-08-08-661-521-9
US-08-08-61-521-44
PCT-US95-01219-44
PCT-US95-01219-44
PCT-US95-01219-44
US-08-561-521-11
PCT-US95-01219-11
PCT-US95-01319-2
US-08-050-050-2
PCT-US95-01030-2
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PCT-US95-01219-4
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Query Match
Best Local Similarity
Matches 140; Conserv
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63.5	63.7	63.7	63.7	63.7	63.7	63.7	64.7	64.8	64.8	65.5	66.3	66.8	67.1	67.3	67.6	67.6	67.6
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US-09-096-244-4	PCT-US96-09448-18	PCT-US95-10053-15	US-08-290-592E-18	US-08-477-989B-86	US-08-472-281A-86	US-08-477-877B-86	US-08-039-198B-10	US-08-465-313-10	US-08-182-067-10	US-09-171-945-19	US-08-767-128-22	US-08-207-169A-2	US-08-232-081B-38	US-08-646-265A-99	US-08-792-824-13	US-08-792-824-10	US-08-792-824-7
Sequence 4, Appli	Sequence 18, Appl	Sequence 15, Appl	Sequence 18, Appl	Sequence 86, Appl	Sequence 86, Appl	Sequence 86, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 19, Appl	Sequence 22, Appl	Sequence 2, Appli	Sequence 38, Appl	Sequence 99, Appl	Sequence 13, Appl	Sequence 10, Appl	Sequence 7, Appli

ALIGNMENTS

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RESULT 1
US-08-561-521-4
                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-4
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                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
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APPLICATION NUMBER: US/08/561,521
FILING DATE:
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COMPUTER READABLE FORM:
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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CITY: San Francisco
STATE: California
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100.0%; Score 746; DB 2; 100.0%; Pred. No. 1.5e-68; ...
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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FILING DATE: 25-JAN-1554
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
NAME: Smith, William J.
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APPLICANT:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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121 YGNYGVYAMDYWGQGTSVTV 140
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                                                 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                              61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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Leger, Olivier J.
Saldanha, Jose
Jones, S. Tarran
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Sequence 9, Application PC/TUS9501219 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 1527
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
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STATE: California
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100.0%; Pred. No. 2.2e-58;
htive 0; Mismatches 0;
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Best Local S
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ADDRESSEE: Townsend and Townsend Khourie and Cr
STREET: One Market Plaza, Steuart Tower, Suite
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NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 25-JAN-1994
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                APPLICANT: OHTOMO, TOShihiko
APPLICANT: SATO, KOH
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
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                   CORRESPONDENCE ADDRESS
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 15270-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                              DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120
                                                                                                                                                                                                                                                                                                                                              DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.
21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leger, Olivier J. Saldanha, Jose Jones, S. Tarran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bendig, Mary M.
Leger, Olivier J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.5%; Score 645; DB 5; I
100.0%; Pred. No. 2.2e-58;
tive 0; Mismatches 0;
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te 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 125;
                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08024253 Patent No. 5785968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
                                GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: MISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
APPLICANT: TOKYOSHI, Sachio
APPLICANT: TOHYA, Yukinobu
APPLICANT: MIKAMI, Takeshi
TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
STREET: 1233 20th Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 53.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQGLEWIGRIDPADGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCA-SAY 119
                                                                                                                                                                                                                                                                                                                                                                                                                    YVN-----QDYWGQGTSVTV 134
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Washington D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 amino acids
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US-08-836-561-31
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TELEFAX: (202) 835-0605
TELEX: 440706 WEGBR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOICCY:
                                                                                                                                                                                                                                                                                                                                 Sequence 31, Application US/08836561 Patent No. 6018032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 116;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/024,253
FILING DATE: 19930301
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 79189/1992
APPLICATE: 28-FEB-1992
ATTORNEY/AGENT INFORMATION:
ANNE: CANTON
                                                                                                                                                                        APPLICANT: ANAZAWA, Hideharu APPLICANT: HANAI, No. 6018032uo APPLICANT: TAKATSU, Kiyoshi TITLE OF INVENTION: Antibody Aga TITLE OF INVENTION: Receptor Al
             ZIR: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                    APPLICANT:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                            121 AW-----LAYWGQGTLVTV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YGNYGYYAMDYWGQGTSVTV 140
   COMPUTER:
                                                                               STATE:
                                                                                                            STREET:
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                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Relace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: CANTOR, Herbert
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                              10036
                                                                                         New York
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                                                                             Ϋ́
                                                                                                         E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                              USA
                                                                                                                                                                                                                                                  NAKAMURA, Kazuyasu
IIDA, Akihiro
                                                                                                                                                                                                                                                                                  FURUYA, Akiko
                                                                                                                                                                                                                                                                                                KOIKE, Masamichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.8%; Score 595; DB 1
82.9%; Pred. No. 3e-53;
ative 8; Mismatches
                                                                                                                                                                   Antibody Against Human Interleukin-5 Receptor Alpha Chain
                                                                                                                                                         106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indels
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                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 70 TELECOMMUNICATION INFORMATION: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Vers: CURRENT APPLICATION DATA: APPLICATION NUMBER: US, FILING DATE: 09-MAY-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 -GGLRLRFFDYWGQGTTLTV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YGNYGVYAMDYWGQGTSVTV 140
                 CLASSIFICATION:
                                APPLICATION NUMBER: US/08/561,521 FILING DATE:
                                                                               SOFTWARE:
                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                       ZIP:
                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 212-790-90-
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
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Local Similarity 82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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                                                                                                                                                                       94105
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                                                                                                                                                                                     USA
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Leger, Olivier J.
Saldanha, Jose
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linear
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09-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 137;
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FILING DATE: 25-JAN-1994 ATTORNEY/AGENT INFORMATION:

Smith,

William L

APPLICATION NUMBER: US/08/186,269A FILING DATE: 25-JAN-1994

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-01219-17
; Sequence 17, Application PC/TUS9501219
; GENERAL INFORMATION:
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Best Local :
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                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/186,269

FILING DATE: 25-JAN-1994

ATTORNEY,AGENT INFORMATION:

NAME: Smith, William L.

REFERENCE/DOCKET NUMBER: 15.270-14

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1.543-9600

TELECOMMUNICATION: 4.15-543-9600
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SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GQRLEWMGRIDPANGYTKYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                      415-543-5043
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-17
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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-561-521-44
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Best Local Similarity
Matches 108; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LENGTH: 142 amino acids
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                          TELEPHONE: 415-543-9600
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                                                                                                                                                                                          NAME: Smith, William L. REGISTRATION NUMBER: 30,223 REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GQRLEWMGRIDPANGYTKYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY 120
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                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                   LENGTH:
                                                                                                                                                        TELEPHONE:
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5840299
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                                                                                 125 amino acids
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                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYY--GNYGVYAMDYWGQGTS 137
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                                                                   20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 25-JA
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                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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Saldanha, Jose
Jones, S. Tarran
                                                                                                                              Conservative
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                                                                                                                                             89.4%;
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89.4%;
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                                                                                                                          2; Mismatches
                                                                                                                      Score 562; DB 5; Length 125; Pred. No. 5.9e-50; 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 562; DB 2; Length 125; Pred. No. 5.9e-50; 2; Mismatches 9; Indels
                                                                                                                      2;
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                                                                                                                    Gaps
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                                              PCT-US95-15716-8
                                                                    RESULT 13
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US-08-348-548-8
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                Sequence 8, Application PC/TUS9515716 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Berdoz, Jose
APPLICANT: Krzechenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
                                                                                                                                                 121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                  117 YGT--SYWFPYWGQGTLVTV 134
                                                                                                                                                                                         60
                                                                                                                                                                                                 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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                                                                                                                                                                                                                                                                                                                                      Match 74.3%;
Local Similarity 80.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DPKFQGKATITADISSNTAYLQLSSLTSEDTAVYYCARGYYYYDSXVGYYAMDYWGQGTX 120
                                                                                                                                                                                 EQGLEWIGWIDPENGNTYYDPKFQGKASITADTSSNTAYLQLSSLASEDTAVYYCA---Y 116
                                                                                                                                                                                                                                                                                                                            113;
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Berdoz, Jose
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                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                                                                                                    Score 554; DB 4; Length 136; Pred. No. 4.3e-49; 6; Mismatches 15; Indels
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                                                                                                                                                                                                            Sequence 11, Application US/08561521 Patent No. 5840299
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                                                                                                                                                                                           GENERAL INFORMATION:
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ZIP: READABLE FORM:

MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM_PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                               TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
                                                                                                                  APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        117 YGT--SYWFPYWGQGTLVTV 134
                                                                                                                                                                                                                                                                                                                                         121 YGNYGYYAMDYWGQGTSVTV 140
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CITY: B
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                                                                                                                                                                                                                                                                                                                                                                                                                               61
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STRANDEDNESS: not
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TELEX: 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/348,548 FILING DATE: 01-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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San Francisco
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Pred. No. 4.3e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application PC/TUS9501219 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 15 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Smith, William L. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
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                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 72.9%; Score 544; DB 2; Score Similarity 82.6%; Pred. No. 3.9e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
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                                                                                                                                                              California
                                                                                                                                                                                                  E: Townsend and Townsend Khourie and Crew One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                           USA
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APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PCLASSIFICATION:
PAPPLICATION: US 08/186,269
FILING DATE: 25-JAN-1994
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9600
TELEPHONE: 415-543-9600
TELEPAX: 415-543-5043
INFORMATION FOR SED ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: molecule TYPE: protein
PCT-US95-01219-11
Search completed: May 7, 2002, 12:23:04 Job time: 175 sec
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                                                                                                                                                                                                                                                                                               Query Match 72.9%; Score 544; DB 5; Length 123; Best Local Similarity 82.6%; Pred. No. 3.9e-48; Matches 100; Conservative 11; Mismatches 10; Indels
                                                                                          121 V 121
                                                                                                                            140 V 140
                                                                                                                                                      0; Gaps
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
     Compugen Ltd.
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:47; Search time 37.68 Seconds (without alignments) 283.026 Million cell updates/sec

Title:
Perfect score:
Sequence: US-09-155-739-4 746

1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 219241

219241 segs, 76174552 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR_68:* pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	5	4	ω	2	_	NO.	Result
455	455.5	456	457	457.5	459	459	460.5	461.5	461.5	462.5	464.5	466.5	467	471	472.5	492	493.5	494.5	498	500	515	521.5	523	539	567.5	570.5	597	603.5	Score	
61.0	61.1	61.1	61.3	1.				61.9													69.0		٠	•	76.1	76.5	0	80.9		Query
140	141	249	138	107	140	135	141	139	115	99	139	139	107	140	114	221	108	268	120	116	115	122	117	120	123	137	136	178	Length	
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PH1498	A39276	S41374	E32513	A27646	HVMSG7	PH1492	JL0076	A27609	PL0246	D37262	MHMS18	PS0024	PH1013	PH1482	A47271	S49220	PH1012	A56446	S03484	S24289	S03482	S06823	S17586	S03471	PH1403	S52445	S04576	S29594	ID	
ig neavy chain v i		ngle chain Fv	heav	heavy chain	Ig heavy chain pre	Ig heavy chain V r	b	Ig heavy chain pre	Ig heavy chain V r	heavy chain	heavy	heavy chain	heavy			Ig gamma-1 chain -		heavy	heavy	gamma	Ig heavy chain V-D	heavy	Ig heavy chain V r	Ig heavy chain V-D	Ig heavy chain V r	Ig heavy chain V r	heavy	Ig gamma chain (WM	Description	

RESULT S04576

N

Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C;Accession: S04576
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dlxon, F.J.;
Eur. J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involv
A;Reference number: S04573; MUID:87133856
A;Accession: S04573; MUID:87133856
A;Molecule type: mRNA
A;Residues: 1-136 <KOF'>
A;Cross-references: EMBL:X14624; NID:952029; PIDN:CAA32777.1; PID:952030
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Superfamily: immunoglobulin V region; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <MAT'>
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT'>

44	43	4 1	40	بر و	38	37	36	35 5	34	33	32	31	30	
439 438	440	440	440.5	441	444	447	451	451.5	452	453	454	454	454.5	
58.8 58.7	59.0	59.0	59.0	59.1	59.5	59.9	60.5	60.5	60.6	60.7	60.9	60.9	60.9	
123 99	446	122	120	140	140	140	135	469	135	140	138	118	133	
NN	N	งผ	N	N	N	2	N	N	N	N	N	N	N	
S20646 C37262	S40295	520643	S41394	PH1488	PH1486	PH1489	PH1494	S37483	PH1493	PH1484	S21810	S25174	PC1155	
Ig heavy chain V r Ig heavy chain V r	gamma	Ig heavy chain V r	heavy	heavy	Ig heavy chain V r	, heavy	heavy	Ig gamma-2a chain	Ig heavy chain V r	Ig heavy chain pre				

ALIGNMENTS

Ig gamma chain (WM65) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 06Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 C;Date: 06Jan-1995 #text_change 05-Nov-1999 C;Date: 06Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999 C;Date: 06Jan-1995 #sequence_revision 06-Jan-1995 A;Crossinited

F;34-117/Domain: immunoglobulin homology <IMM>

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PH1403
Ig heavy chain V region (clone micro m- 46-6, 46-12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: PH1403
C;Accession: M: Minagon T · Haniwara. S.: Kimoto, H.; Shigemoto, K.; Tanig
A;Residues: 1%123 <SHI>
                                                                                                                       R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta
J. Exp. Med. 176, 1209-1214, 1992
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A)Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                            ia virus.
                                                                                                                   A;Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region precursor - mouse (;Species: Mus musculus (house mouse) C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000 C;Accession: $52445 R;Berdoz, J.; Kraehenbuhl, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Restdues: 1-137 <BER>
A;Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged gen
A;Reference number: S52445
A;Accession: S52445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKCSWVMFFLMAVVTGVNSEVOLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                 Heavy chain variable (VH) region diversity generated by VH gene replacement in
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                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                     YGT--SYWFPYWGQGTLVTV 135
                                                                                                                                                                                                                                                                                                                                                                                                                             EQGLEWIGWIDPENGNTYYDPKFQGKASITADTSSNTAYLQLSSLASEDTAVYYCA---Y 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVRPGALVKLSCKASGFNIKDYYMYWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQGLEWIGWIDPENGDTQYASKFQGKATMTADTSSNTTYLQLSSLTSEDTAVYYCT---- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EOGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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Pred. No. 8.4e-43;
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Ig heavy chain V region (E8) - mouse (fragment)
c;Speciles: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S17586
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D. J. Mol. Biol. 221, 455-462, 1991
                                                                                                                                                           RESULT
S17586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983 A;NOte: this sequence was determined from the differentiated gene R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J. Immunol. 129, 2554-2558, 1982
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire A;Reference number: 807453; MUID:83058021
A;Accession: 807453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 1-43 < ROC2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 7-120 < ROC1>
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A;Introns: 16/1
A;Introns: 116/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-118/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                       61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR----GWLRRDAMDYWGQGTSVT 116
                                                                                                                                                                                                                                                                                                                                                                                 80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
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89.3%;
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94.9%;
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Pred. No. 4e-40;

 3; Mismatches

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2;
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A;Reference number: S17586; MUID:92015240
A;Accession: S17586
A;Accession: S17586
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <MYL>
A;Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig heavy chain V region (clone IIc) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
C;Accession: S06823
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of mur
A;Reference number: S06813; MUID:90064531
A;Accession: S06823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Biochemical implications from the variable gene sequences of an anti-cytochrome
                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-99/Domain: immunoglobulin homology <IMM>
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Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #C;Accession: S03482; S07453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-122 <MIL>
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                                                                                  RESULT
S03482
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                                                                                                                                                       TV 120
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                                                                                                                                                                                                                                                                                      EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHEWVKQRPEQGLEWIGRIDPANGNTK 60
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                                                                                                                                                                                                                                                                                                                                                                       69.9%;
                                                                                                                                                                                                                                                                                                                                                                       Score 521.5; DB 2;
Pred. No. 1.4e-38;
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                   26-Feb-1998 #text_change
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                                                                    mouse (fragment)
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                                     101;
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A; Note: this sequence was determined from the differentiated gene R; Rocca-Serra, J.; Mazle, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire A; Reference number: S07453; MUID:83058021
A; Accession: S07453
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                               K,Moncharmont, B. MBL Data Library, Se A,Description: Cloning and sequencing A,Reference number: $24287 A,Accession: $24289
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A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
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A;Accession: S03482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig gamma chain V region (JS34/32) - mouse C;Species: Mus musculius (house mouse) C;Date: 20-Feb-1995 #sequence_revision 20:C;Accession: S24289
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A; Residues: 10-115 < ROC1>
                                                                                                                                                                                                                                                        A;Cross references: EMBL;X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: immunoglobulin
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                                                                                                                                                                                                                                     F;14-97/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
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Best Local Similarity
                                                                                                                                Query Match 67.0%;
Best Local Similarity 81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DPKFQGKATITTDTSSNTAYLQFSSLTSEDTAVYYCARGTTVGR------DYWGQGTTLT 114
                                                  21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
1 VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
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                                                                                                       Conservative
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                                                                                                                                Score 500; DB 2; Length 116; Pred. No. 9.5e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               September 1991 ng of the cDNA coding
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Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally idential A;Reference number: A56446; MUID:95229583
                                                                                                                                             A;Cross-references: GB:U20617
C;Keywords: heterotetramer; in
                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-268 <TAN>
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A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMN>
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A:Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se A:Reference number: S07453; MUID:83058021
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A; Residues: 10-120 <ROC1>
A; Cross-references: EMBL: X07144
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A;Accession: S03484
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                                                                          Query Match
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                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
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1, .
                                                                                                                                        heterotetramer; immunoglobulin
                              Conservative
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                                                  66.3%;
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                              8; Mismatches
                                                  Score 494.5; DB 2
Pred. No. 6.8e-36;
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Pred. No. 1.5e-36;
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                                                                   DB 2;
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                           Indels
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F:121-221/Domain: C region #status predicted <C: F:139-203/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                           C;Keywords: immunoglobulin F;1-120/Domain: V region **status predicted <VRG>
                                                                                                                                                                                                                        A; Experimental source: strain Balb/c C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: 237502; NID: g541778; PIDN: CAA85732.1; PID: g541779
                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-221 <KIP>
                                                                                                                                                                                                                                                                                                                                                            A; Description: Cloning and A; Reference number: $49220 A; Accession: $49220
                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-108 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1 C;Superfamily: immunoglobulin V region; immunoglobu C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Kipp, B.; Becker, W.P.; Schlaak, M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S49220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A; Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig heavy chain V region (clone 17p.73) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1012
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PH1012
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A;Accession: PH1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
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          96;
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       Conservative
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79.3%;
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                          Score 492; DB 2; Pred. No. 9.2e-36;
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Pred. No. 3.3e-36;
     Mismatches
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                                               Length 221;
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20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79

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Ig heavy chain V region (clones 36-35[TG] and X7-TG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1482; PH1495
R;Glusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation.
d for somatic mutation.
d; For somatic mutation.
d; Reference number: PH1482; MUID:93171820
A;Reference number: PH1482
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
A;Experimental source: hybridoma cell
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli G;Date: 21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995 C;Accession: A47271 R;Lesley, S.A.; Patten, P.A.; Schultz, P.G. R;Lesley, S.A.; Patten, P.A.; Schultz, P.G. Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993 A;Title: A generatic approach to the generation of antibodies with enhanced catalytic action, Reference number: A47271; MUID:93165660 A;Accession: A47271
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C; Species: synthetic
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                Query Match
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YG--GSYYFDYWGQGTTLTV 138
                 YGNYGVYAMDYWGQGTSVTV 140
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Search completed: May 7, 2002, 12:23:47 Job time: 198 sec

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Maximum Match 100%
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 Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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ช. - พ.	Wari T., Rajewsky K., e NPb family of 2a variable region."; LONED FROM A HYBRIDOMA 3-NITROPHENYL)ACETYL coed through a collaboration and the EMBL outstation and the EMBL outstation ire no restrictions on its ts content is in no way age by and for commercial ://www.isb-sib.ch/announce/	.; Mus.	homo sapien mus musculu carassius a mus musculu mus musculu homo sapien

Query Match Best Local Similarity

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Score 464.5; DB 1; Pred. No. 8.1e-38;

Length 139;

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                                                                                                                                                                                                                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
SIGNAL 1
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21-JUL-1986 (Rel. 01, Last sequence upd
15-JUL-1999 (Rel. 38, Last annotation u
IG HEAVY CHAIN V REGION 9367 PRECURSOR.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=82152818; PubMed=6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                        PIR; A02028; HVMSG7
                                                                                                                                                                                                                                                                                                   EMBL; J00493; AAA38128.1; -.
                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                            "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; Science 216:309-311(1982).
                                                                                                                                                                                                                                                                                                                                                                                                              Science
                                                                                                                                                                                                                                                                                                                                                                                                                                              Capra J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090
        121
                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HV02_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YGNYGVYAMDYWGQGTSVTV 140
                                                                     61
                                                                                                          1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
    YG--GSYDFDYWGQGTPLTV 138
                          YGNYGYYAMDYWGQGTSVTV 140
                                            GQGLEWIGYINPGNGYINYNEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHY 120
                                                                EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                     MGWSFIFLFLLSVTAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGS---SYFDYWGQGTTLTV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EOGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAYYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91;
                                                                                                                                                Similarity
                                                                                                                                                                                          140
                                                                                                                                    Conservative
                                                                                                                                                                                                      140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                               20
                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                        140
15514 MW;
                                                                                                                                                                                                               140
                                                                                                                                            61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                             Score 459;
Pred. No. 2.
                                                                                                                                                                                                            IG HEAVY CHAIN V REGION 93G7
                                                                                                                                                                                       25A4CBBE31DA5CE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 AA
                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                             DB 1;
?.7e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                     Length 140;
                                                                                                                                  Indels
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                                                                                                                                  2;
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                                                                                                                                1;
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QΨ
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Best Local S
Matches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                         Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HV03_MOUSE
         (NPB ANTIBODIES).
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_MOUSE MULTIPOPER STANDARD; PRT; 137 AA PO1755; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 1G HEAVY CHAIN V REGION S43 PRECURSOR.
                                                  "Heavy chain variable region contribution antibodies: somatic mutation evident in a Cell 24:625-637(1981).
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01747;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG HEAVY CHAIN V REGION 36-65.
                                                                                                                                           Bothwell A.L.M., Paskind M.,
                                                                                                                                                                   MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
NON_TER 120 120
                       1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  idiotype response of the strain A mouse.*;
Eur. J. Immunol. 12:1023-1032(1982).
-1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL
DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE
CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED
SEGMENT, JH2.
PIR. A02028; HYMSG7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=83131846; PubMed=6186498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marshak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The genetic basis of antibody production: the dominant anti-arsonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYG--GSYYFDYWGQGTTLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13307 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.0%; Score 425; DB 1; 68.3%; Pred. No. 4.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches
                                                                                               contribution to the
                                                                                                                                      Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FF04E4A167B654AF CRC64;
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                                                                          gamma
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                                                                                               NPb family
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                                                                       variable
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                                                                       region.";
                                                                                               of.
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RESULT
HV48_M
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Best Local
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PIR; A02033; HVMST7.
InterPro; IPR03006; Ig_vHC.
InterPro; IPR0303596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                HV48_MOUSE STANDARD; PRT; 138 AA. P03980; P03980; 23-OCT-1986 (Rel. 02, Created) 23-OCT-1986 (Rel. 02, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A02038; GZMS43.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A02038; G2MS43
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                                                                                                                                             Proc.
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                                                                                                                                                                                                                           Gilliam A.C., Shen
                                                                                                                                                                   delta in an IgD-secreting
                                                                                                                                                                                                            Tucker P.W.;
                                                                                                                                                                                                                                                   MEDLINE=84248078; PubMed=6429663;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                        (llegitimate recombination generates a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGRY----FDYWGQGTTLTV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00047; ig; 1.; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J00539; AAA38172.1; -.
                                                                                                                                             Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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20
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118
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                                                                                                                                               Sci. U.S.
                                                                                                                                                                                                                                Α:
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54
68
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                                                                                                                                                                                                                                  Richards
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                                                                                                                                                 plasmacytoma.";
S.A. 81:4164-4168(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 422.5;
Pred. No. 8.
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JH2
BY S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG HEAVY CHAIN V REGION S43.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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E
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                                                                                                                                                                                                                                  Blattner
                                                                                                                                                                                        class switch
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                                                                                                                                                                                                                                F.R.,
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                                                                                                                                                                                                                                                                                                HV09_MOUSE STANDARD; PRT; 11/ AA P01753; P11271; 21-JUL-1986 (Rel. 01, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
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                                                                                                                                              RELATED GENES THAT COULD PIR; B02034; HVMS61.
                                                                                                                                                                          "Heavy chain variable region contribution antibodies: somatic mutation evident in a Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                         MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                   STRAIN=C57BL/6;
                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                    DOMAIN
                                                                              CHAIN
                                                                                       SIGNAL
                                                                                               Immunoglobulin
                                                                                                                            InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                                                                   -!- MISCELLANEOUS:
                                                                                                                                                                                                                 Bothwell A.L.M., Paskind
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                      120 YYGNYGVYAMDYWGQGTSVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP
                                                                                                                                                                                                                                                                                            musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                    YYDWF-----VYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-EG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGWSYIILFLVATATDVHSQVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRP
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
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                                                        IG HEAVY CHAIN V REGION 186-1.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                             FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.
                                                                                                                                                                                                                Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                          ENCODE
                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     748157E4C6907B8E CRC64;
   16191A088CB17F5A
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                                                                                                                                                         REGIONS OF NPB ANTIBODIES
                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                      region.";
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Query Match

Best Local Similarity

55.1%;

Score Pred.

411; No.

1; DB 1; 8.9e-33;

Length 117;

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RESULT 8
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HV15_M
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Best Local
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InterPro; iPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by a cloned B-cell lymphoma: a single copy of the by two adjacent CH genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Simultaneous expression of immunoglobulin mu and delta heavy chains
by a cloned B-cell lymphoma: a single copy of the VH gene is shared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=82222262; PubMed=6806821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G HEAVY CHAIN V REGION BCL1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A02042;
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                                                                                                                                                   121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                                             61 AKSLEWIGVISTYNGNTSYNOKFKGKATMTVDKSSSTVHMELARLTSEDSANLYCAR--Y
                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                            1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                       EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                      MGWSCIIFFLVATATGVHSQVQLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J00494; AAA38130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSSTAYMQLHSLTSEDSAVYYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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136
136 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136
15078 MW; 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           53.1%;
                                                                                                                                                                                                                                                                                                                                                                                     23;
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                                                                                                                                                                                                                                                                                                                                                                             Score 396; DB 1; Length 136; Pred. No. 2.9e-31; 3; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG HEAVY CHAIN V REGION BCL1
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         HV49_
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HV49_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                              unrearranged VH gene segments.";
Cell 40:271-281(1985).
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P01750;
21-JUL-1986 (
21-JUL-1986 (
15-JUL-1999 (
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
This SWISS-PROT entry is copyright.
                                                                                    "Developmentally controlled and tissue-specific expression
                                                                                                                                     MEDLINE=85099340; PubMed=2578321;
                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                  UI-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, 01-JAN-1988 (Rel. 06, 15-JUL-1999 (Rel. 38, 
                                                                                                                                                                                                                                                                                                                                                                           P06328;
01-JAN-1988
                                                                                                                 Yancopoulos G.D., Alt F.W
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSEI RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES PIR; A02032; HVMS02.
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Pfam: PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibodies: somatic m
Cell 24:625-637(1981)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 102 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Pred. No. 4.8e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3. BY SIMILARITY.
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG HEAVY CHAIN V REGION 145 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                    antibodies: somatic mutation evident in Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HV10_MOUSE
P01754; P11270;
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=81234548; PubMed=6788376; Bothwell A.L.M., Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090
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                                                                                                                                                                                                                                                      MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAYYFCAR 117
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                                                                                                                non-profit institutions as long and this statement is not removed.
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IGv; 1.
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No. 4.8e-31;
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BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
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InterPro;
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Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
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SMART; SM00406; IGv; 1.
Immunoglobulin V region;
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                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION 23 PRECURSOR.
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antibodies: somatic mutation
                                                                                                                                                                                                                                                     Bothwell A.L.M., Paskind M.,
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                             SEQUENCE
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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                            Baltimore D.;
                                                                                                                                                                                                                                                               MEDLINE=81234548; PubMed=6788376;
                                                                                                                                                                                                                                                                          STRAIN-C57BL/6;
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                                                                                                                                                                                                      -!- MISCELLANEOUS:
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COMPLEMENTARITY-DETERMINING
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FRAMEWORK 1
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                                                                                                                                                                                                                                 contribution to the NPb family of
                                                                                                                                                                                                                                                       Reth M., Imanishi-Kari T., Rajewsky K.,
                                                         COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
                                                                             COMPLEMENTARITY - DETERMINING 1.
FRAMEWORK 2.
                                                                                                  IG HEAVY CHAIN V REGION FRAMEWORK 1.
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                                                   BY SIMILARITY.
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Best Local
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SMART; SM00406; IGv;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression unrearranged VH gene segments.";
Cell 40:271-281(1985).
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01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION VH558 A1/A4 PRECURSOR.
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       STANDARD;
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No. 6.7e-30;
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 3.
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       PRT;
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Best Local :
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REVISIONS.

Zakut R., Cohen J., Givol D.;

Zakut R., Cohen J., Givol D.;

Nucleic Acids Res. 8:4839-4840(1980).

-i- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED

FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-81053741; PubMed=6253904;

MEDLINE-81053741; PubMed=6253904;

Zakut R., Cohen J., Givol D.;

"Cloning and sequence of the cDNA corresponding region of immunoglobulin heavy chain MPCII.";

Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01745;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence of the control of the
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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"Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40(1980).

-i- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION J558.
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-!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
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(Rel. 01, Last sequence update)
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RESULT 15
HV1C_HUMAN
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     ALCONDUCTOR REPORT OF THE STATE OF THE STATE
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Best Local S
Matches 75
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InterPro; IPRO03006; Ig_wHC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 1.
Pfam; PF00047; ig; 1.
IMMUNOQ10bulin V region.
NON_TER 121 121
                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; I.
SMART; SM00406; IGv; I.
IMmunoglobulin v region; Signa
SIGNAL 1 19
CHAIN 20 147 I
MOD_RES 20 20 F
DISULFID 41 115
CONFLICT 53 54
CONFLICT 53 54
CONFLICT 125 168 V
CONFLICT 125 168 V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-83065234; PubMed-6815656;

MEDLINE-83065234; PubMed-6815656;

MEDLINE-83065234; PubMed-6815656;

Method T.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,

Bell L.O., Gould H.J.;

Bell L.O., Gould H.J.;

Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line.";

""" Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYIC_HUMAN STANDARD; PRT; 14/ AA. P01744; P01744; P1-1986 (Rel. 01, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) IG HEAVY CHAIN VII REGION ND PRECURSOR (FRAGMENTS).
DISULFID
CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN.
PIR; A02026; E1HUND.
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.1-36,
Marcel bekker, New York (1978).
-I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 20-147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 75; Conserv
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     16491 MW;
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                                                          T -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                                                                                IG HEAVY CHAIN V-I REGION ND. PYRROLIDONE CARBOXYLIC ACID.
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        948F9F72A5366C20 CRC64;
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Best Local (
 129
                     124 YGVYAMDYWGQGTSVTV 140
                                           69
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                                                                                               9 FLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIG 68
DYSYTLDVWGQGTTVTV 145
                                          RIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-----EGYYGN 123
                                                                                    FLVAAATRVHSQTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVG
                                                                                                                                         Similarity
                                                                                                                                Conservative
                                                                                                                                          50.7%;
                                                                                                                                25;
                                                                                                                                          Score 378.5; DB 1
Pred. No. 1.5e-29;
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                                                                                                                                                    DB 1;
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                                                                                                                                                    Length 147;
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Search completed: May 7, 2002, 12:32:34 Job time: 565 sec

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                   Pred. No. is the nu score greater than and is derived by a
  Score
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1: /SIDSB/gcgdata,
2: /SIDSB/gcgdata,
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Query
Match
                                                                                                                                   is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:

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SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:

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SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:

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     Length
        DB
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                                                                                        SUMMARIES
  Description
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83. 5 82. 7 82. 7 81. 5 81. 1 81. 0 81. 0 81. 0 81. 0 81. 0 81. 0 80. 4 80. 5 80. 6 80. 2 80. 3

AAR13658 AAR26981 AAR65163 AAR47207 AAW35133 AAW86805 AAW70625 AAW10231 AAW70673

R. pipiens recombi Variable Light dom Humanised murine a CDR-grafted light Anti-VEGF humanise TF8-5G9 CDR-grafte Protein encoded by Variable Light dom Humanised murine a Humanised anti-alp Human VI consensus

Consensus human li Human variable lig Human consensus fr Human consensus se pUC-RV1-PM1a. Syn pUC-RV1-PM1a. Syn

Interleukin-6 spec

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453 451.5 451.5

475.5 471.5 460.5 460.5 456 455 455 455 455 453.5

AAR13050 AAR78970 AAR93159 AAR06252 AAR26983 AAW26797 AAR85495 AAY26800 AAR81322 AAW26800

Amino acid sequenc Anti-gp54 MAb T16 Humanized VLA-4 an Humanised alpha-4 Murine OKT4A light

Anti-gp54 MAb ScFv(FWP51). Variable region of (FRP51)-ETA fusion Murine monoclonal CD4-specific CDR-g

Synt

chain variab

FWP51 fusion prote Human REI monoclon Human/murine IL-1

AAW10233 AAW70703 AAW86804 AAW70623 AAW87455 AAB62087

ALIGNMENTS

X P P P X	DR:	Y P S	Y P X	PR	XX PF	X PD	X T X Z	XX	80	2	X X	×	XEX	DŢ	XX	×	ij	RESULT
New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.	WPI; 1995-269276/35.	Bendig MM, Jones TS, Leger OJ, Saldanha J;	(ATHE-) ATHENA NEUROSCIENCES INC.	25-JAN-1994; 94US-0186269.	25-JAN-1995; 95WO-US01219.	27-JUL-1995.	W0951979U-A1.		Chimeric Homo sapiens.	Objects Win miscelling	antibody engineering.	Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;	Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.	02-APR-1996 (first entry)	WAKOT271;	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	AAR81321 standard; Protein; 106 AA.	LT 1

110 110 110

508 508 508 508 508 488 488

100.0 100.0 100.0 90.4 90.4 90.4 90.4 86.8 86.8 86.8

106 106 126 126 126 126 126 126 127 128

116 116 116 116 116 120 20 20

AAR81321 AAW22412 AAW22413 AAW21328 AAR81326 AAR81332 AAW22409 AAY29911 AAY29911 AAY29916 AAR60627

Humanized anti-VLA
Humanised alpha-4
Humanised alpha-4
Mouse anti-VLA-4 antibo
Human VLA-4 reshap
Alpha-4 integrin m
Human WCP-3 and mu
Human IP-10 and mu
Artificial synthet
ME1-14 light chain

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AAW22412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence encodes the humanized mouse antibody 21.6 light chain variable region, La, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and 2C AAQ998892) regions are linked to human constant regions in the 2C construction of a humanized antibody against VLA-4. The 5' and 3' C ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors CC containing human kappa or gamma-1 constant regions. In the humanized Clight chain, amino acids L45, L49, L58 and L69 in the humanized CC light chain, amino acids L45, L49, L58 and L69 in the humanized CC vR framework are replaced by the amino acid present in the equivalent CC position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric CC can be used for inhibiting adhesion of a leukocyte to an endothelial CC cell and for treating inflammatory diseases such as multiple CC cerebral traumas, meningitis or encephalitis. The antibodies can corebrating anti-lairous antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
Misc-difference 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis;
                                                                                                       Misc difference
                                                                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric Mus musculus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-1997
                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised alpha-4 integrin antibody 21.6 VL La.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW22412 standard; Protein; 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dermatitis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                        synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens;
                                                                                                  /note= "REI framework region 45
                                                                                                                                                                              /note= "21.6
35..49
                                                                                                                                                                                                                                  24..34
/label= CDR1
                                           /note= "REI Lys-45 is substd. by Lys of mouse 21.6 \text{ VL}, important in supporting the
                                                                                                                                                                                                                                                                                   /note= "REI framework region 1"
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                           /label= FR2
                                                                                                                                                                                                                                                                                                                 /label= FR1
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                           CDR2 loop"
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                                                                                                                                                                                                      complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myocardial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 562; DB 16;
Pred. No. 6.9e-37;
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Sequence

106 AA;

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This polypeptide, designated La, comprises the light chain variable cregion (VL) of a humanised alpha-4 integrin antibody 21.6. It is CC composed of complementarity determining regions (CDRs) from the VL CC region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody C21.6 and a modified human REI framework. It can be expressed in CC mammalian host cells following PCR amplification and mutagenesis CC of appropriate fragments of mouse and human DNA sequences. The CC to produce a claimed humanised 21.6 VH (see AAW22413) can be used CC to produce a claimed humanised 21.6 antibody that is useful in the CC manufacture of a medicament for treating asthma, atherosclerosis, CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid CC arthritis, transplant rejection, graft versus host disease, tumour CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial CC ischaemia, and acute leukocyte mediated lung injury. The antibody CC may also be used in the affinity purification of alpha-4 integrin CC for use as a vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibody has a CC half-life in the human circulation essentially equivalent to that CC of naturally occurring human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; Fig 6; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Uses of humanised alpha-4 integrin antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             asthma, atherosclerosis, AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-297879/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ATHE-) ATHENA NEUROSCIENCES INC
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103
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97..106
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/note= "21.6 complementarity determining region
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21.6 VL, important in supporting the CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "REI Thr-69 is substd. by Arg of mouse 21.6 VL, involved in antibody-antigen binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "REI Thr-106 substd. by Lys, more typical of human kappa light chain J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "REI Gln-104 substd. by Glu, of human kappa light chain
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Best Local Similarity
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                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                               asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
                                                                                                                                                                                                                                                                                                    Protein
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Chimeric Homo sapiens;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised alpha-4 integrin antibody 21.6 VL version La.
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                                         21-NOV-1996;
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        NEUROSCIENCES INC
                         9508-0561521
                                                                                                                                                                /label= CDR2
/note= "21.6
77..108
                                         96WO-US18807
                                                                                                            /label= CDR3
/note= "21.6 |
117..126
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44..54
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                                                                                                                                                                                                                                                                                                            /label= Leader
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                                                                                                                                                                                                                                                        "REI framework region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polypeptide, designated La, comprises the light chain variable region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also AAW22412). It is composed of complementarity determining regions in the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody 21.6 and a modified human REI framework. It can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-297879/27.
N-PSDB; AAT74788.
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bendig MM,
                                                                                                                                                                                                                                                                                    Mouse anti-VLA-4 antibody 21.6 light chain variable region.
                                                                                                                                                                                                                                                                                                                                         AAR81328;
                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                         Humanized antibody; leukocyte adhesion
          Region
                                                                Region
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                                                                                                                                                                                                                                            antibody engineering.
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                                                                35..49
           50..56
                                                                                                                                                                                      Location/Qualifiers
                                      /note=
                                                   /label= FR2
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                           "mouse light region 2"
                                                                                           "mouse light
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                                                                                 chain variable region 1"
                                      chain variable
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/label= CDR2

AAR81326;

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AAR81326
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                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
AAR81326 ştandard; Protein; 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-idiotype antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ATHE-) ATHENA NEUROSCIENCES INC
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    region 4"
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determining region 2"
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Pred. No. 1.1e-32;
6; Mismatches 6;
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modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and
                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents the mouse antibody 21.6 light chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned CDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5′ and 3′ ends of the mouse cDNAs are
                    to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating
anti-idiotype antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ99889
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77..10
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      The sequence represents the human reshaped antibody 21.6 light chain variable region against leukocyte adhesion molecule VIA-4. Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VIA-4. The 5' and 3' ends of the
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                                                                                                                       Bendig MM,
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Pred. No. 1.2e-32;
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(See AAQ99895-98)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mediated lung injury; therapy
                                                                                                                                                             77..10
                                      /note= "complementarity
117...126
                                                                                                 109..116
                                                                                                                                                                                                                                                                                                                                                                /note= "framework region
                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                   /label= FR4
                                                                                                                                       /label=
                                                                                                                                                                                                   /label= CDR2
                                                                                                                                                                                                                                         /note= "framework region
                                                                                                                                                                                                                                                              /label= FR2
                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                          /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Leader
/note= "framework region
                                                                              /Label=
                                                                                                                    /note= "framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.4%;
                                                                                                                                                                              "complementarity determining
                                                                                                                                                                                                                                                                                                       "complementarity determining region
                                                                              CDR3
                                                                                                                                            FR3
                                                                                                                                                                                                                                                                                                                                                                                       FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 508; DB 16;
Pred. No. 1.2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₿
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                                                                                                                    region
                                                           determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises the light chain variable region (VL) of mouse anti-alpha-4 integrin monoclonal antibody 21.6. The complementarity determining regions (CDRs) of the 21.6 VL can be Complementarity determining regions (CDRs) of the 21.6 VL can be Complementarity determining regions (CDRs) of the 21.6 VL can be Complementarity determining regions (CDRs) of the 21.6 VL can be Complementarity determining a claimed humanised 21.6 Complementarity and a claimed humanised 21.6 Complementary between the complementarity and a chaimed humanised 21.6 Complementary determining a disease selected from asthma, atherosolerosis, AIDS, Complementary determining a disease, inflammatory bowel disease, rheumatoid arthritis, transplant rejection, graft versus host disease, tumour complementaries, atopic dermatitis, pooriasis, myocardial complementaries, and acute leukocyte mediated lung injury. The antibody complementaries are vaccine or an immunogen. It is also useful for generating idiotypic antibodies. The humanised antibodies of the complementaries humanised antibodies of the complementaries that the complementaries are the complementaries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
16-SEP-1999
                            WO9946392-A1
                                                                                  Homo sapiens
                                                                                                                             Chemokine; tumour; viral; antigen; fusion protein;
                                                                                                                                                                                       17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                  AAY29913 standard; Protein; 359
                                                                                                                nmune response; HIV; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               equivalent to that of naturally occurring human antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 68; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma, atherosclerosis, AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uses of humanised alpha-4 integrin antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-297879/27.
N-PSDB; AAT74759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ATHE-) ATHENA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09718838-A1
                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 AA;
                                                                                                                                                          and murine scFv38 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US18807
                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leger OJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 508; DB 18; Pred. No. 1.2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saldanha J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein 3 (MCP-3) and human Muc-1; (2) human interferon induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human SDF-1 and human Muc-1; (5) human IP-10 and HIV gpl20; (7) human MDC and HIV gpl20; and (8) human SDF-1 and HIV gpl20. The fusion proteins, and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays fumour antigen epitopes and fine mapping of tumour antigen epitopes and fine mapping of fumour antigen epitopes and fine mapping of invention.
12-MAR-1998;
                          12-MAR-1999;
                                                            16-SEP-1999
                                                                                        WO9946392-A1
                                                                                                                        Synthetic.
                                                                                                                                                                                                  Chemokine; tumour; viral; antigen; fusion protein;
                                                                                                                                                                                                                                  Human IP-10 and murine scFv38 fusion protein.
                                                                                                                                                                                                                                                                     17-NOV-1999
                                                                                                                                                                                                                                                                                                                              AAY29911 standard; Protein; 361 AA
                                                                                                                                         ds snw
                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                   AAY29911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                      LMMune response; HIV; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 118-119; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                         233 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 292
                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                   (first entry)
                            99WO-US05345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0077745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 488; DB 20; Pred. No. 1.1e-30; 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                   cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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RESULT 1
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DRX PRAKET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein 3 (MCP-3) and human Muc-1; (2) human interferon induced protein 10 (IP-10) and human Muc-1; (3) human interferon induced protein 10 (IP-10) and human Muc-1; (4) human SDF-1 and human MCP-3 and HIV gpl20; (7) human MCP-3 and HIV gpl20; (7) human MCP-3 and HIV gpl20; (7) human MCP-3 and nucleotide sequences encoding them, can be used for producing an immune response, e.g. an effector T cell immune response. They can also be used for treating cancer or treating or preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays for identifying unknown tumour antigen epitopes and fine mapping of tumour antigen epitopes. The present sequence represents a fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 115-116; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kwak LW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH &
                                                                                   12-MAR-1998;
                                                                                                                                           16-SEP-1999
                                                                                                                                                                        W09946392-A1
                                                                                                                                                                                                                                            Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
                                                                                                                                                                                                                                                                         Artificial synthetic construct protein SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                 AAY29916;
                                                                                                                                                                                                                                                                                                                                                              AAY29916 standard; Protein; 374 AA
                           Kwak LW, Biragyn A;
                                                                                                                12-MAR-1999;
                                                                                                                                                                                                                                immune response; HIV; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from the present invention.
                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                     295
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                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biragyn A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                   98US-0077745
                                                                                                                99WO-US05345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 488; DB 20;
Pred. No. 1.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes fusion proteins comprising a chemokine and a tumour antigen or HIV antigen. Specifically claimed fusion proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and tuman Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human SDF-1 and HIV gpl20; (6) human IP-10 and HIV gpl20; (6) human SDF-1 and HIV gpl20; (7) human MDC and HIV gpl20; and HIM gpl20; (1) human sDF-1 and MIV gpl20. The fusion proteins, and nucleotide sequences encoding them, and be used for producing an immune response, e.g. an effector T cell commune response. They can also be used for treating gancer or treating cor preventing HIV infection. The fusion proteins and/or nucleotide sequences can be used in in vitro diagnostic assays, as well as in screening assays for identifying unknown tumour antigen epitopes and fine mapping of tumour antigen epitopes. AAY2916 and AAZ21168 are sequences given in the SEQ ID LISPING in the present invention but which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fusion polypeptides comprising a chemokine and a tumour antigen or HIV antigen, used for treating cancers or treating or preventing HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JUN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody; tumour
                                                                                                                                                                                                                                                                                                                                                                                                     ME1-14 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR60627 standard; Protein; 128 AA
                                              N-PSDB; AAQ73537
                                                            WPI; 1994-316669/39
                                                                                             Bigner DD, Carrel S,
                                                                                                                                                                                                                                  14-MAR-1994;
                                                                                                                                                                                                                                                                                                    WO9421294-A.
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                             (BIGN/) BIGNER D D. (CARR/) CARREL S.
                                                                                                                                                                                                  19-MAR-1993;
                                                                                                                                                                                                                                                                    29-SEP-1994.
                                                                                                                             (ZALU/) ZALUTSKY M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 digmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not mentioned further within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 AA;
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                                                                                                                                                                                                  93US-0033864
                                                                                                                                                                                                                                    94WO-US02724.
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84.9%;
                                                                                               Zalutsky MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 488; DB 20; Pred. No. 1.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Method of treating solid or cystic tumours with antibodies - by administering monoclonal antibody Mel-14, having Fc deleted,

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RESULT
AAR13050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EX CCCCCXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                 21-DEC-1989;
21-DEC-1990;
21-DEÇ-1990;
Jolliffe LK,
                                                                                                   W09109966-A.
                                                                                                                           Region
                 (ORTH ) ORTHO PHARM CORP.
                                                                  21-DEC-1990;
                                                                                   11-JUL-1991.
                                                                                                                                           Region
                                                                                                                                                            Region
                                                                                                                                                                            Region
                                                                                                                                                                                            Region
                                                                                                                                                                                                             Region
                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                     complementarity determining region.
                                                                                                                                                                                                                                                                                                              variable region;
                                                                                                                                                                                                                                                                                                                             CD4-specific CDR-grafted light chain.
                                                                                                                                                                                                                                                                                                                                                                             AAR13050 standard; Protein;
                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                               27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cystic tumours.
See also AAR60626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of the ME1-14 light chain. The protein monoclonal antibody which can be administered to treat solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        using injection or deposition in the cyst cavity
                                                                                                                                                                                                                                                                                                                                                                                                                   21 digmtqspsslsas1ggkvtitckasqdinkylawyqhkpgkgprllmhytst1qpgips 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                              (first entry)
Zivin RA,
                               89GB-0028874.
90WO-GB02017.
90WO-GB02018.
                                                                  90WO-GB02015
                                                                                                                                                                                            /label
                                                                                                                                                                                                             /label
                                                                                                                          /label= framework region 4
133..234
                                                                                                                                                                             /label
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                   /label=
                                                                                                                                                                  /label= framework
                                                                                                                                                                                                                                                                                                              antibody;
                                                                                                                                                                                                                                     /labe
                                                                                                                                                                                                                                                    /label= signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.6%;
                                                                                                                                                                                    _ CDR 2
                                                                                                                                                                                                   l= framework region
                                                                                                                                                                                                                     l= CDR 1
                                                                                                                                                                                                                                    l= framework region
                                                                                                                  kappa constant domain
                                                                                                                                                   CDR 3
Pulito VL,
                                                                                                                                                                                                                                                                                                             OKT4A; heavy chain; CD4;
                                                                                                                                                                                                                                                                                                                                                                               234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 481; DB 15;
Pred. No. 1.6e-30;
9; Mismatches 8;
                                                                                                                                                                  region
Adair
JR,
Athwal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is
or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR78970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                   neutralising heavy metals
                                                                            New polypeptide(s) which bind heavy metals, esp. mercury - derived from monoclonal antibodies, used for detecting, removing, adding or
                                                                                                                             WPI; 1995-275415/36.
                                                                                                                                                                                                                                                 03-AUG-1995.
                                                                                                                                                     Lopez 0,
                                                                                                                                                                          (BION-) BIONEBRASKA
                                                                                                                                                                                                  27-JAN-1994;
                                                                                                                                                                                                                         27-JAN-1995;
                                                                                                                                                                                                                                                                         WO9520607-A.
                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; heavy metal; mercury; variable region;
                                                                                                                                                                                                                                                                                                                                                     Light chain variable region for monoclonal antibody 23F8.
                                                                                                                                                                                                                                                                                                                                                                                                       AAR78970;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAR78970 standard; Protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is an example of a CDR-grafted light chain of the invention. The constant regions are based on sequences of the human kappa constant domain, the signal sequence is derived from murine MAD B72.3 and the CDR sequences are based on the murine OKT4A light chain CDRs. The recombinant antibody encoded by this sequence has affinity for CD4 similar to that of OKT4A.
                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 8; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New CD4 specific recombinant - complementarity determining region grafted antibody for treating graft rejection and T cell
                                                                                                                                                                                                                                                                                                                      light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ12633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-222914/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 diqmtqspsslsasvgdrvtitckaspdinnylnwyqqtpgkapklliyytstlqpgvps 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90;
                                                                                                                    AAQ97508
                                                                                                                                                    Wagner FW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ12627-Q12632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                  94US-0187407
                                                                                                                                                                                                                          95WO-US01199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.6%;
                                                                                                                                                    Wylie DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 475.5; DB 12; Pred. No. 7.2e-30; 8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
```

7;

Hybridoma antibodies have been produced with the spleen cells of BALB/c mouse that had received multiple injections of mercuric in reacted with glutathione to produce a mercuric ion coordinate

ions

Claim 23; Page 67-68; 106pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     guanidine isothiocyanate. First strand cDNA synthesis was catalysed by MuLv reverse transcriptase. The primers used for cDNA synthesis were complementary to the 5' end of the CH1 domain of the heavy chain expressed by the hybridoma of interest, or to the 5' and of the C kappa domain. Some of the primers used for cDNA synthesis are shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the cariable region of a particular antibody polypeptide was also used for PCR amplification of that variable region, in conjunction with an appropriate v-region primer. In addition, the VH primer AAQ97518 was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences of the PCR amplified nucleotides were determined. These are given an AAQ97918-Q97510 and the deduced AA sequences in AAR79241-R79250 & C AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45 and in the claims are different from the descriptions in the sequence listings are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hemocyanin (KLH). Eight hybridomas (1110, 4010, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 1011, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T cell activation; complementarity determining region; CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine monoclonal antibody K20 kappa chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR93159 standard; Protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                covalent compound which was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F
                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; light chain; kappa; variable region; K20; integrin; beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-OCT-1996 (first entry)
                                                             Region
                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                             /note=
89..94
                                                                                                                                                  /note=
57..88
                                                                                                                                                                                                                                           /note=
50..56
                                                                                                                                                                                                                                                                                                                                 /note=
35..49
                                                                                                                                                                                                                                                                                               /label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "framework region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
/label= CDR3
/note= "complementarity determining region"
                                                                                                                                                                                                         /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                     /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= FR1
                                                                                                                       /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.9%;
83.2%;
                                                                                                                                                                                                                                                                    "framework region'
                                                                                        "framework region"
                                                                                                                                                                              "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                         "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 471.5; DB 16; Length 107; Pred. No. 7.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23F8, 2D5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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Вb
                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                          AAR06252
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody K20. The antibody recognises the beta I subunit (CD29) of integrins and inhibits activation and proliferation of peripheral T cells induced by anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target for humanisation; the humanisation may be useful as an immunosuppressant. In the humanisation process, the complementarity determining regions (CDRs) of a human antibody with framework regions 70-95% homologous to those of K20 were replaced by the K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanisation of non-human immunoglobulin variable regions prodn. of humanised antibodies, esp. K20, e.g. as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-1994;
                                01-AUG-1990
                                                                                                                         Variable region of murine AHT 107 light chain.
                                                                                                                                                10-DEC-1990 (first entry)
                                                                                                                                                                                               AAR06252 standard;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 2A; 39pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-162083/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bernard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROT-) PROTEINE PERFORMANCE SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INRM ) INSERM INST NAT SANTE &
                                                       EP380068-A.
                                                                                                    Interleukin-2 receptor; IL-2;
                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cervoni MF,
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94FR-0010858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94FR-0010858
          90EP-0101351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= J_kappal
                                                                                                                                                                                              protein; 128
                                                                                                                                                                                                                                                                                                                                                          82.7%;
81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lefranc MP,
                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                               Score 465; DB 17;
Pred. No. 2.3e-29;
0; Mismatches 10;
                                                                                                     tumour necrosis factor; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDICALE
                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                     Length 108;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                               Gaps
```

0;

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PR 04-DEC-1989; 89US-0441702.
PR 24-JAN-1989; 89US-0301216.
XX

PA (MOLE-) MOLECULAR THERAPEU.

XX

PA (MOLE-) MOLECULAR THERAPEU.

XX

PY Zerler B;

XX

N-PSDB; AAQ05556.

XX

PT Expression vectors for producing chimeric monoclonal antibodies -
PT which express human constant region and non-human variable region

XX

PT Expression vectors for producing chimeric monoclonal antibodies -
PT which express human constant region and non-human variable region

XX

Disclosure; p; English.

XX

MAbs comprising mouse CH and CL constant regions whith human

CC variable regions may be used to create mouse/human hybrid MAbs,

CC variable regions may be used to create mouse/human hybrid MAbs,

CC variable regions may be used to create mouse/human hybrid MAbs,

CC which have a longer serum half-life. Method can be used to produce

XX

XX

SQ Sequence 128 AA;

81.9%: Score 460 5: DR 11: Length 128.
```

Query Match 81.9%; Score 460.5; DB 11; Length 128; Best Local Similarity 76.6%; Pred. No. 6e-29; Matches 82; Conservative 18; Mismatches 6; Indels 1; Gaps 1;

Search completed: May 7, 2002, 12:22:25 Job time: 246 sec

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Title:
Perfect score:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-339-582-4
US-08-888-366-22
US-08-235-838-16
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US-08-465-4738-11
US-08-465-4738-11
US-08-602-725-29
US-08-602-725-211-9
US-08-437-6428-17
US-08-437-6428-18
US-08-437-6428-18
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Sequence 5, 1
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11, Appl
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NESULT 1 US-08-561-521-7 US-08-561-521-7 Sequence 7, Application US/0856 Patent No. 5840299 GENERAL INFORMATION: APPLICANT: Bendig, Mary M. APPLICANT: Seldanha, Jose APPLICANT: Seldanha, Jose APPLICANT: Jones, S. Tarran TITLE OF INVENTION: Humani: TYPE: Possible Form: APPLICATION SECO STATE: California COUNTRY: USA ZIP: 94105 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati OPERATIOR SYSTEM: PC-DOS SOFTWARE: PatentIn Relea CURRENT APPLICATION NUMBER: US/O FILING DATE: APPLICATION NUMBER: US/O FILING DATE: 25-OAN-1994 ATTORNEY/AGENT INFORMATION: NAME: Smith, William L. REFIGENEZ/JOCKET NUMBER: 30/O TELEFRA: 415-543-5043 INFORMATION FOR SEQ ID NO: 7 SEQUENCE CHARACTERISTICS: SEQUENCE SEQUENCE CHARACTERISTICS: SEQUENCE SEQ	28 444.5 79.1 29 444.5 79.1 30 443.5 78.9 31 443.5 78.9 32 443.5 78.9 33 443.5 78.9 34 443.5 78.9 36 440.5 78.4 38 440.5 78.4 40.5 78.4 410.5 78.4 42 440.5 78.4 43 438.5 78.0 45 438.5 78.0
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Leukocyte	Sequence 71, Appl Sequence 6, Appli Sequence 34, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 39, Appli Sequence 39, Appli Sequence 39, Appli Sequence 39, Appli Sequence 47, Appli

Query Match
Best Local Similarity

100.0%;

Score 562; DB 2; Pred. No. 1e-45;

Length 106;

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TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 15-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 25-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran
                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   Local Similarity
                                                                                                               1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
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One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                                                                             Sequence 5, Application GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
10 amino acids
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                                                                                                              APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT: Saldanha, Jose APPLICANT: Jones, S. Tarran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                        TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
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STATE: California
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                                                                                                                                                                                                                                                                                                     RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106
                                                                                                                                                                                                               Application PC/TUS9501219
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
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FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
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                                     CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4
                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/
FILING DATE: 25-JAN-1995
                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                             CITY: San Francisco
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Local Similarity 88.7%;
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APPLICATION NUMBER: US/08/561,521 FILING DATE:
                                                                                                                                                                            COUNTRY:
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US-08-561-521-15
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Best Local Similarity 88.7
Matches 94; Conservative
                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-TAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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INFORMATION FOR SEQ ID NO:
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                TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30.2
REFERENCE/DOCKET NUMBER:
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APPLICATION NUMBER: |
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: Townsend and Townsend Khourie and Crew
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APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco
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CHARACTERISTICS:
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                                   415-543-5043
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Pred. No. 1.3e-40;
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TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-15
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                                                                    Matches
                                                                                             Query Match
Best Local 9
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TELEPAX: 415-543-5043
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bendig,
APPLICANT: Leger,
APPLICANT: Saldanha
APPLICANT: Jones,
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                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                              TELEPHONE: 415-543-9600
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
Local Similarity nes 94; Conserv
                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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Jones, S. Tarran
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Leger, Olivier J.
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                                                                                       90.4%;
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                                                                       Score 508; DB 5; Length 126; Pred. No. 1.3e-40; 6; Mismatches 6; Indels
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US-08-339-582-4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 25-JAN-
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
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                                                                        61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                           81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco
                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                           94; Conservative
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amino acid
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                                                                                                                                                                                         Score 508; DB 5; Length 126; Pred. No. 1.3e-40; 6; Mismatches 6; Indels
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Patent No.

GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

Bigner, Darell D. Zalutsky, Michael R. Carrel, Stefan

Sequence 4, Application US/08339582 Patent No. 5558852

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US-08-888-366-22
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                                                                                                                                                                                                                                              Patent No. 5972656
GENERAL INFORMATION:
APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/08888366 Patent No. 5972656
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                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                              NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,864
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31,665 REFERENCE/DOCKET NUMBER: 54
                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLLTFGGGTKLEIK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                              55402
                                                                                                                                                                Minneapolis
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                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 89; Conserv
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               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     APPLICANT: APPLICANT:
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                   TITLE OF INVENTION: Recombinant Antibodies Specific for a TITLE OF INVENTION: Growth Factor Receptor NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
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LENGTH: 107 amino acids
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PRIOR APPLICATION NUMBER: US 08/187,407
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                                                                                                                    ZIP: 10532
                                                                                                                                  COUNTRY:
                                                                                                                                                     STATE:
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APPLICATION NUMBER:
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                                                                                                                                                                   Hawthorne
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Zwickl, Markus
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 US/08/235,838
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Pred. No. 2.7e-37;
9; Mismatches 8;
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INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wels, Winfried S. APPLICANT: Hynes, Nancy E. APPLICANT: Harwerth, Ina-Maria APPLICANT: Groner, Bernd APPLICANT: Hardman, No. 593953; APPLICANT: Zwickl, Markus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
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                     FILING DATE: 31-JAN-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05-FEB-:
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 91-810079.3
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227
                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/828,832 FILING DATE: 31-JAN-1992
                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 07901-6940
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Summit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
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                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                APPLICATION NUMBER: US/08/465,473B FILING DATE: 5 June 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     564 Morris Avenue
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                       05-FEB-1991
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                                             GB 91-810079.3
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Patent No. 5571894
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                 TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 1:
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APPLICANT:
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          FILING DATE: TBA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hardman, No. 5571894man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 16
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SEQUENCE CHARACTERISTICS:
                                                                                                                                               FILING DATE: 05-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
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                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATOR TO THE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CLD. OTDRET: 7 Skyline Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                   TELEPHONE:
                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIBA-GEIGY Corporation
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                                                                                                                                                                                                                            31-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant Antibodies Specific for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ina-Maria
                                                                                                                                                                                                                                                                                                                       US/08/235,838
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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-235-838-11
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-08-465-473B-11
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
REGISTRATION NUMBER: 22,640
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                                                                                                                                                                                                                             TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OF SEQUENCES: 34
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APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-M
                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
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                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RESGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
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CLASSIFICATION:
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nes 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08 FILING DATE: 5 June 1995
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                                                                   ; ORGANISM:
US-08-602-725-29
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/GB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION UMBER: GB 9317423
APPLICATION UMBER: GB 9317423
FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER NUMBER OF SEQUENCES: 40
                                                                                                 FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                   NAME: SADOFF, B.J.
REGISTRATION NUMBER: 366
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 02-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
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TOPOLOGY: lin
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5965710
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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BATES, PAUL A
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STEWART, LORNA MD
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                                                                                 Hukan REI light chain
                                                                                                                                                               linear
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                                                                                                                  N-terminal
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 80.9%;
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Score 454.5; DB 2
Pred. No. 1.1e-35;
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                 DB 2;
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Matches

Conservative

80

Mismatches

Indels

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Search completed: May 7, 2002, 12:23:04 Job time: 175 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
 SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_votent:*
12: sp_virus:*
13: sp_vertebrate
14: sp_unclassifi
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Gapop 10.0 , Gapext 0.5
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746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                     sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                    sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                           473505
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match I	Length	DB	Ħ	Description
1	589	79.0	468	11	Q99L31	Q99131 mus musculu
2	494.5	66.3	473	11	Q99L25	mus
ω	480	64.3	109	11	Q9JL85	Bum
4	478	64.1	473	11	Q9D8L4	Bru
ъ	425.5	57.0	463	11	Q99LC4	aum t
6	412	55.2	117	11	Q9QXE9	Q9qxe9 mus musculu
7	388.5	52.1	118	11	Q9Z1C4	Q9z1c4 mus musculu
æ	387	51.9	117	11	Q9QXF0	mus
9	383.5	51.4	110	11	Q9JL77	Q9j177 mus musculu
10	380	50.9	111	11	09D9B8	Q9d9b8 mus musculu
11	376.5	50.5	109	11	Q9JL75	Q9j175 mus musculu
12	375.5	50.3	114	11	Q9JL81	Q9j181 mus musculu
13	371.5	49.8	124	4	Q9UL92	Q9u192 homo sapien
14	369	49.5	484	11	Q99LA6	mus
15	367	49.2	150	4	Q9Y298	homo
16	366.5	49.1	500	4	Q9BRV0	homo
17	361	48.4	157	4	095978	095978 homo sapien
18	353	47.3	119	տ	Q9GYZ2	schi
19	350	46.9	119	4	Q9UL94	Q9u194 homo sapien

2000 2000 2000 2000 2000 2000 2000 200	20 21 22 24
302.5 302.5 301 301 301 301 301 302.5 302.	348.5 343 340.5 338 324.5
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298 150 120 120 119 119 1113 1131 1131 1131 1231 121 121 124 124 124 124 124 124 124 12	110 125 487 117 116
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ALIGNMENTS

RESULT Q99L25 ID Q AC Q DT 0	OC OC OC OX OX OX RP RP RA RL DR SO OU Be: Hari	RESULT Q99L31 ID Q AC Q DT Q DT Q DT Q OS P
LIT 2 ,25 ,29 ,099L25 PRELIMINARY; PRT; 473 AA. ,099L25; ,01-JUN-2001 (TrEMBLrel. 17, Created)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. StrausDerg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. StrausDerg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. StrausDerg R.; SEQUENCE 468 AA; 51681 MW; 96352328B3332ADB CRC64; SEQUENCE 468 AA; 51681 MW; 96352328B3332ADB CRC64; SEQUENCE 468 AA; 51681 MW; 96352328B3332ADB CRC64; SEQUENCE 114; Conservative 9; Mismatches 13; Indels 4; Gaps Matches 114; Conservative 9; Mismatches 13; Indels 4; Gaps	1 PRELIMINARY; PRT; 468 AA. 199131; 1-JUN-2001 (TrEMBLrel. 17, Created) 1-JUN-2001 (TrEMBLrel. 17, Last sequence update) 1-JUN-2001 (TrEMBLrel. 17, Last annotation update) IMILAR TO RIKEN CDNA 1810060009 GENE. Tus musculus (Mouse).

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Best Local Similarity
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Best Local :
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                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TremBLrel. 15, Created)
01-OCT-2000 (TremBLrel. 15, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
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InterPro; IPR003596; Ig_v.
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1; -. nrqRRqR7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
Mus musculus (Mouse).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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88 TITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
                                                                 28 AELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKA 87
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                                               1 AELVKPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEWSWVFLFFLSVTTGVHSQVQLQQSDAELVKPGASVKISCKVSGYTFTDHTIHWVKQRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQGLEWIGYIYPRDGSTKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGGS 120
                                                                                                                                                                                                                                      SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                          109 AA;
                                                                                                                  Conservative
                                                                                                                                                                                                           109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                          TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                           109
                                                                                                                                                                                          11944 MW;
                                                                                                                               64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                8;
                                                                                                               Score 480; DB 11;
Pred. No. 3.8e-41;
8; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 494.5; DB 11;
Pred. No. 8e-42;
9; Mismatches 24;
                                                                                                                                                                                        DFE615FE6CED4EDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 AA
                                                                                                                                           DB 11; Length 109;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashinaki Y. .
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Piam; PF00047; Ig; 4.
SMART; SMODAGG.
                                                                                                                                                                                                                                                                                                                                 SMART; SM00409; IG; 2.

SMART; SM00407; IGc1; 3.

SMART; SM00406; IGv, 1.

SMART; SM00410; IG_like; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

SEQUENCE 473 AA; 51699 MW; 9DED5
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STRAIN=CS7BL/60; TISSUE-PANCREAS;
MEDLINE-21085660; PubMed=11217851;
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 1810060009RIK PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1924014; 1810060009Rik.
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01-JUN-2001
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121 -- DYDWFA--YWGQGTLVTV 136
                                  121 YGNYGVYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                         Loca1
                                                                                                                                                      1 MEWSWVFLFLLSVTAGVHCQVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRP
                                                                                                                                                                      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                        GQGLEWIGKIGPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGY
                                                                                          EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK007918; BAB25349.1;
                                                                                                                                                                                                                              64.1%; Score 478; DB 11;
Similarity 67.1%; Pred. No. 3.7e-40;
19: Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                 9DED57A514475FBB CRC64;
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EMBL; BCOC
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                                                                                                                                                                                                                                                                                                                                   O9QXE9;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                 Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPAT
                                                                                                                                                                                                                                                                                                                                                                                                     Q9QXE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                  NON_TER
                                                                                                                                        InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                    SEQUENCE
                                                                                                                                                                                           EMBL; AJ225174; CAB65237.1;
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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            20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGNYGYYAMDYWGQGTSVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEWIWIFLFILSGTAGVHSQVQLQQSGAELARPGASVRLSCKASGYTFTGYGVSWVKQRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y-SYDLFA--YWGQGTLVTV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tted (FEB-2001) to the EMBL/GenBank/DDBJ databases. BC003435; AAH03435.1; -. NCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                Similarity
                                                                                                    117
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
                                                                                                      13000 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.0%;
                                                55.2%;
                                    ; Score 412; DB 11;
; Pred. No. 3.1e-34;
14; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 425.5; DB 1
Pred. No. 7.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                      CDDE2AF84D499734 CRC64;
                                                                                                                                                                                                                      AND MAJOR HISTOCOMPATIBILITY
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                                                                                                                                                                                                                                                                                                                                                                                                      117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muridae;
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                                                              Length
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SCCOPPINA
SCCOPP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                  O9QXFO:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Matis L.M., Evans M.J.; "Humanized porcine VCAM-specific monoclonal antibodies w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
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                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                           Q9QXF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IgG2/G4 constant regions block human leukocyte binding
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 V 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 SVTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY-----YAMDYMGQGTSVT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TOKFRGKATLTADKSSSTAYMOLSSLASEDSAVYYCARRTVGGYF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCARE---GYYGNYGVYAMDYWGQGT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77;
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118
118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                     Rodentia;
                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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Pred. No. 7.5e-32;
                                         Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90EEC559D31EC4FC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                   Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                    B
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                                              Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ç
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Best Local
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Best Local
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                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                           Malkiel S., Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TremBLrel. 15, Created)
01-OCT-2000 (TremBLrel. 15, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                         EMBL; AF206029; AAF69327.1;
                                                                                                                                                                                                                                                                                                                                                      STRAIN-DBA/2;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9JL77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9JL77;
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Submitted (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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InterPro; IPR003596; Ig_v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
90 TADŢSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
                                                       30 LVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKATI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDKDYY-----FDYWGQGTTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
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                           3 EVRPGASVKLSCKASGYTFTSSWMHWAKQRPGQGLEWIGEIHPNSGHTNYNEKFKGKATL
                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                    SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mens A., Rademaekers A., Specht C., Koelsch E.;
mitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

MILLARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                PF00047; ig; 1.; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٧٢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPKFQGKATITADISSNTAYLQLSSLISEDIAVYFCARE-GYYGNYGVYAMDYWGQGISV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ225171; CAB65236.1; -.
                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115
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                                                                                                                                                           110 AA;
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117 AA; 13060 MW; D816AD0858A47E4C CRC64;
                                                                                       Conservative
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                                                                                                                                                                          110
                                                                                                                                                          12138 MW; 2EDE81FB5862C9AF CRC64;
                                                                                                   51.4%;
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63.1%;
                                                                                       15;
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                                                                                                 Score 383.5; DB 1
Pred. No. 2.2e-31;
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Pred. No. 1e-31;
                                                                                     Mismatches
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                                                                                                              DB 11; Length 110;
                                                                                       18;
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(TrEMBLrel. 15, PRELIMINARY;

Created) PRT;

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                                                                                                    RESULT 11
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RC MEDLINE-21085660; PubMed-11217851;
RX Arakawa T., Shinagawa A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RX Arakawa T., Hara A., Fukunishi Y., Kondo S., Yamanaka I.,
RX Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RX Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RX Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RX Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RX Kachi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RX Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RX Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RX Sakai K., Okido T., Fruuno M., Aono H., Baldarelli R., Barsh G.,
RX Sakai K., Okido T., Fruuno M., Aono H., Baldarelli R., Barsh G.,
RX Barki Y., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RX Arakincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RX Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RX Asaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RX Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RX Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RX Hayashizaki Y.,
Wilming L.,
RX Hayashizaki Y.,
Wilming L.,
RX Hayashizaki Y.,
RX Hayash
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Best Local Similarity
Q9JL75 I
Q9JL75;
Q1-OCT-2000 (
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SMART; SM00409; IG; 1.

SMART; SM00406; IGv; 1.

SMART; SM00410; IG_like; 1.

SEQUENCE 111 AA; 11976 MW;
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01-JUN-2001
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ADULT MALE TESTIS CDMA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:1700110111, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AK007163; BAB24877.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003600; InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interPro; IPR003599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           !- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                          14 VTGVNSEVQLQQSGAELVKPGASVKLSCTASGENIKDTYIHCVKQRPEQGLEWIGRIDPA 73
                                                                                                                                                                                                                74 NGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
                                                                                                                                                                                                                                                             1 MTGVHSQVQLQQSGPELVKPGASVKISCKASGYAFSSSWMNWVKQRPGKGLEWIGRIYPG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                   DGDTNYNGKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAR 104
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig.
; Ig_like.
; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                 50.9%; Score 380; DB 1 70.2%; Pred. No. 5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17, Created)
17, Last sequence update)
17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              874DDF7BD98BD7B2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
                                                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Length 111;
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RESULT
Q9JL81
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      Matches
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Q9JL81;
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                       Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BALB/C;
Malkiel S., Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malkiel S., Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
                                                                                                                                                                                                       InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: TO IMMUNOGLOBULIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF206031; AAF69329.1;
                                                                                                                                                                                                                                                                           AF206025; AAF69323.1;
                                                                                                                                                                                     SM00406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
      Similarity 61.6
69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                   IPR003006;
                                                                                                                    114
114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA,
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                                                                                                                                                                                     IGV;
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                                                                                                                    114
12829
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12118 MW;
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                           50.3%;
                                                                                                                                                                                                                                                   Ig_MHC.
                                                                                                                    WW;
      21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 376.5;
Pred. No. 1.1e
18; Mismatches
Score 375.5; DB 11;
Pred. No. 1.5e-30;
Pred. No. 1.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FF65E441BBF936A6 CRC64;
                                                                                                                    404885FDE6BA56F8
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                                                                                                                                                                                                                                                                                                                       MAJOR
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hes 18;
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                                                   DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muridae;
                                                                                                                                                                                                                                                                                                                    HISTOCOMPATIBILITY
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      Indels
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae;
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                                                     114;
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      1;
                                                                                                                                                                                                                                                                                                                    COMPLEX
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      Gaps
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RESULT
Q9UL92
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Q99LA6
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NON_TER
SEQUENCE
                                                              O99LA6;
O1-JUN-2001 (TrEMBLrel. 17, Creat
O1-JUN-2001 (TrEMBLrel. 17, Last
O1-JUN-2001 (TrEMBLrel. 17, Last
UNKNOWN (PROTEIN FOR MGC:6319).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Myosin-reactive autoantibodies
fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                        Q99LA6
                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clin. Immunol. Immunopathol. 87:184-192(1998)
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE
                      NCBI_TaxID=10090;
                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003006;
                                                                                                                                                                               114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
:| | ||:||:||| |||:||| |||:|||
LTVDKSSSTAYWQLSSPTSEDSAVYYCARSNYYGS-SLYYFDYWGQGTTLTV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WGQGTSVTV 140
                                                                                                                                                                                                                           EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKAT
                                                                                                                                                                               WGQGTLVTV 122
                                                                                                                                                                                                                                                DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAM------DY 131
                                                                                                                                                                                                                                                                       EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF035022; AAD56258.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.C.
                                                                                                                                                                                                                                                                                                                                                                                                          SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003596; Ig_WHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                         124
124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                         124
13580 MW;
                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                              49.8%;
                                                                                                                                                                                                                                                                                                                                        .88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13,
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                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                               Pred. No. 4.1e-30;
                                                                                                                                                                                                                                                                                                                                        Score 371.5;
                                Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                          1BAAACBD96ACD2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in rheumatic carditis
                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                             annotation
                                                                                        sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalis N.N.,
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                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae;
                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HISTOCOMPATIBILITY COMPLEX
                                                                           update)
                                  Muridae;
                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berney
                                                                                                                                                                                                                            GLYVVVPAAFSRFDY
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                        Length
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                                            Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGION
                                   Murinae;
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RESULT 15
Q9Y298
ID Q9Y298
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DE IGG VH
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Matches 67
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Best Local :
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SEQUENCE
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98322155; PubMed-9657749;
Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VIII inactivation:
"G44 monoclonal antibody derived from a hemophilia A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
IGG vH PROTEIN PRECURSOR (FRAGMENT).
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003495; AAH03495.1; -
SEQUENCE 484 AA; 52567 MW; 8EAEA4F9BCF582FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blood 92:496-506(1998).
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     119
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                                                   121 YGNYGVYAMDYWGQGTSVTV 140
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                                                                                                                                                                                                                                                                                                                                             y Match 49.2%; Score 367; DB 4; Local Similarity 51.4%; Pred, No. 1.5e-29;
                                                                                                65 EWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity tes 67; Conserv
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                                                                                                                                                                                                             1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60
                                                                                                                                                                                                                                         1 MKCSWVMFELMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
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---- PPDAFDIWGQGTMVTV 134
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150 AA;
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illarity 49.3%;
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150
16031 MW; 563D164AB22802D5 CRC64;
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; Pred. No. 4e-29;
28; Mismatches 39;
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Search completed: May 7, 2002, 12:31:42 Job time: 628 sec

OM protein - protein search, using sw model Run on: May 7, 2002, 12:23:47; Search time 37.68 Seconds (without alignments) 214.291 Million cell updates/sec GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

US-09-155-739-7 562

Title: Perfect score: Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues

Searched:

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	5	4	ω	2		No.	Result	
412	412.5	•	414	414.5	5.	418.5	419.5	•	421.5	424.5	426	429.5	429.5	435.5	439.5	439.5	439.5	•		443	443.5	443.5	446.5	452	463.5	7	479	488	Score		
73.3		73.6		73.8			74.6						٠	77.5						•	78.9		9	0		85.1		86.8		Query	ф
106	108	108	124	131	109	123	108	108	108	125	107	127	110	108	108	107	107	94	107	103	129	108	107	97	125	106	104	104	Length DB		
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PC2397	B49047	K1HUSW	40336	S40352	31998	S40331	K1HURY	K1HUAG	Klhuly	S40333	S36275	S40367	S44118	139154	K1HUAU	PL0271	PL0269	33730	L0272	26332	S52789	K1HURE	PL0270	H1064	09365	33936	S26329	26330			
anti-tetanus toxin	Ig kappa chain V r	kappa		kappa		kappa	_		kappa	kappa	_		Ig kappa chain V-J	kappa chain				kappa	kappa	light		_	_	Ig light chain V r		Ig kappa chain V r		Ig kappa chain V r	Description		

410.5 · 73.0 108 2 S44122 Ig kappa chain V r 410.5 73.0 109 2 S31981 Ig kappa chain V r 409.5 72.9 129 1 KIHUWR Ig kappa chain pre 409 72.8 107 1 KIHUWR Ig kappa chain V-I 408.5 72.7 130 1 KIHUWE Ig kappa chain V-I 407.5 72.5 141 2 A49134 Ig kappa chain V-I 405.5 72.2 117 2 S46371 Ig kappa chain V-I 405.5 72.1 108 2 S30521 Ig kappa chain V-I 404.5 72.1 12 S46371 Ig kappa chain V-I 405.5 72.2 117 2 S46371 Ig kappa chain V-I 404.5 72.1 12 S40334 Ig kappa chain V-I 404.5 72.1 108 2 S30521 Ig kappa chain V-I 404.5 72.1 108 2 S30521 Ig kappa chain V-I 403.5 71.8 127 2 S45264 Ig lambda chain V-I 403.5 71.8 127 2 S35264 Ig kappa chain V-I 403.5 71.8 127 2 S35264 Ig kappa chain V-I 403 71.7 117 2 S4253 Ig kappa chain V-I 403 71.7 117 2 S4253 Ig kappa chain V-I 403 71.7 117 2 S4253 Ig kappa chain V-I	45	44	43	42	41	40	39	38	37	36	<u>3</u> 5	3 4	33	32	31	30
108 2 S44122 Ig kappa chain 109 2 S31981 Ig kappa chain 129 1 KIHUWK Ig kappa chain 107 1 KIHUWK Ig kappa chain 108 1 KIHUWE Ig kappa chain 141 2 S40365 Ig kappa chain 141 2 A49134 Ig kappa chain 117 2 S46371 Ig kappa chain 118 2 S30521 Ig kappa chain 132 2 S40334 Ig kappa chain 137 2 S40343 Ig kappa chain 107 2 S16264 Ig light chain 117 2 S43528 Ig kappa chain 117 2 S43263 Ig kappa chain 118 1 KIHUHU Ig kappa chain 118 1 KIHUHU Ig kappa chain	402.5	403	403	403.5	403.5	403.5	404.5	405	405.5	407.5	408.5	408.5	409	409.5	410.5	410.5·
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chain	к1нини	S42263	S43528	S11240	S36264	PH1063	S40334	S30521	S46371	A49134	S40365	K1HUWE	K1HUAR	K1HUWK	S31981	S44122
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ALIGNMENTS

RESULT 2 \$26329 Ig kappa chain V region - mouse C:Species: Mus musculus (house mouse) C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000 C:Accession: \$26329 R:Stark, S.E.; Catcn, A.J. J. Exp. Med. 174, 613-624, 1991 A:Title: Antibodies that are specific for a single amino acid interchange in a protein a prot	Query Match 86.8%; Score 488; DB 2; Length 104; Best Local Similarity 85.6%; Pred. No. 1.3e-35; Matches 89; Conservative 8; Mismatches 7; Indels 0; Gaps 0; Qy 1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60	RESULT 1 \$26330 If kappa chain V region - mouse C;Specles: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000 C;Accession: \$26300, R;Stark, S.E.; Caton, A.J. J. Exp. Med. 174, 613-624, 1991 A;Title: Antibodies that are specific for a single amino acid interchange in a protei A;Reference number: \$26309; MUID:91341421 A;Reference number: \$26309; MUID:91341421 A;Accession: \$2630 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-104 <sta> A;Cross-references: EMBL:X59185; NID:g52316; PIDN:CAA41895.1; PID:g1334063 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology <imm></imm></sta>
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C;Accession: S09365
R;Feddersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene segn A;Reference number: S09365; MUID:90098844
                                                                                                                                                                                         C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;33-107/Domain: immunoglobulin homology <IVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
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A; Residues: 1-125 <FED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene A;Reference number: A33936; MUID:89282831
A;Accession: C33936
                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
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A; Residues: 1-106 <MEE>
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Best Local :
    18 DIOMTOSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 77
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                                                                                                                   POCGT
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                          1 DIOMTOSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                               82.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.1%; Score 478; DB 2; 83.0%; Pred. No. 9.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Mismatches
                                                                                                                 Pred.
                                                                                                                                   Score 463.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 479; DB 2; Length 104; Pred. No. 7.8e-35;
                                                                                             Mismatches
                                                                                                               No. 2e-33;
                                                                                                                                   DВ
                                                                                         10;
                                                                                                                                2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 106
                                                                                                                                Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                         Indels
                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                       Gaps
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    δÃ
                                                B
                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: heterotetramer;
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-107 <SHL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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A; Residues: 1-97 <TIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                              Matches
                                                                                                                                                                     Query Match
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61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                  Local Similarity
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                           79.4%;
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F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining
F;98-107/Region: framework 4
                                                                                                                                                                                                                                                                                                                                                             F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                  F; 24-34/Region: complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PL0231; MUID:90111618
A;Accession: PL0270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Experimental source: B cell, strain [NZB x NZW]F1 C:Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: PH0971; MUID:92381444
A; Accession: PH1064
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R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;16-90/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RFSGSGSGRDYTFTISSLQPEDIATYYCLOYDNLWTF 97
1 DIQMTQSPCSLSASLGDKVTITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60
                                                        1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin
                                                                                                                                                Score 446.5; DB 2
Pred. No. 5.1e-32;
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Pred. No. 1.6e-32;
                                                                                                                          Mismatches
                                                                                                                                                                             DB 2;
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                                                                                                                       Indels
                                                                                                                                                                                Length 107;
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Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.;
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in my
A;Reference number: S52789
A;Reference number: S52789
A;Status: preliminary
A;Molecule type: mENA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758589; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterofetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Contents: annotation; X-ray crystallography, 2.0 angstroms C;Comment: This is a Bence Jones protein.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 14, 4943-4952, 1975
A; Title: The molecular structure of a dimer composed of the variable portions of A; Reference number: A90392; MUID: 76039968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A;Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom vollstaendige Aminosaeuresequenz des Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain V-I region (Rei) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 *sequence_revision 24-Apr-1984 *text_change
C;Accession: A91663; A01873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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A; Map position: 2p12-2p12
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A; Residues: 1-108 < PAL>
A; Residues: 1-108 < PAL>
A; Note: the C region of this chain has the Inv (1,2) marker
A; Epp, O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: A91663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
                           Similarity
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  Conservative
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81.1%;
                        78.9%;
10;
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                        Score 443.5; DB 2
Pred. No. 1.1e-31;
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Pred. No. 9.4e-32;
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     Mismatches
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                                                    Length 129;
                                                                                                                                                                                                                                                                                                                                                                      peculiarities in myeloma
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A;Reference number: PL0231; MUID:90111618
A;Accession: PL0272
A;Molecula to the control of the c
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A; Residues: 1-103 <572>
A; Residues: 1-103 <572>
A; Cross-references: EMBL: X59191; NID: g52321; PIDN: CAA41901.1; PID: g1334066
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                  C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig kappa chain V region (anti-DNA, 6B8VK) - mouse (fra:\ent) (;Species: Mus musculus (house mouse) (c;Species: Mus musculus (house mouse) (c;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000 (c;Accession: PL0272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332; S26331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N; Alternate names: Ig kappa chain V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-107 <SHL>
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F;98-107/Region:
                                         F;89-97/Region:
                                                                              F;57-88/Region:
                                                                                                                       F;50-56/Region:
                                                                                                                                                                     F; 35-49/Region:
                                                                                                                                                                                                               F;24-34/Region:
                                                                                                                                                                                                                                                             F;16-90/Domain:
                                                                                                                                                                                                                                                                                                       F;1-23/Region: framework
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Best Local :
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Exp. Med. 174, 613-624, 1991
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                                    complementarity-determining
                                                                                                                                                                                                                                                    immunoglobulin homology < IMM>
                                                                              complementarity-determining
framework 3
                                                                                                                                                                          framework 2
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77.7%;
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Pred. No. 9.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Gaps

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F;57-88/Region: II
F;89-97/Region: cr
F;98-107/Region:
                                                                                                                                                                                                                                         Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0269
C:Accession: PL0269
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein,
J. Exp. Med. 171, 255-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618
A:Reference number: PL0231; MUID:90111618
A:Residues: 1-107 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-3/Region: framework 1
F:16-90/Domain: immunoglobulin homology <IMM>
F:36-40/Region: framework 2
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A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unl A;Reference number: A33730; MUID:89367325
A;Accession: E33730
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A; Residues: 1-94 <LAW>
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C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
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                                                                                                                         ;57-88/Region: framework 3;89-97/Region: complementarity-determining
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Best Local :
                     Query Match
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framework 2
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78.5%;
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; Pred. No. 1.7e-31
11; Mismatches 1
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Pred. No. 1.6e-31;
                  Score 439.5;
               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 107;
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               2;
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               Length 107;
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                                                                                                                                                  A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Residues: 1-108 <SCH>
A;Residues: 1-108 <SCH>
A;Residues: 1-108 <SCH
A;Rote: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager,
Blophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones
A;Reference number: A90729; MUID:77022433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C;Accession: A9163; A01862; S02573
                                        R;Steiner, V.; Chang, J.Y. FEBS Lett. 222, 6-10, 1987
                                                                                          A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement
                                                                                                                                                                                                                                                                                                                                                                                                                    R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1
A;Title: Die Primaerstruktur einer monoklonalen
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R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A; Title: Chemical modification of the carboxyl groups of protein substrates enhances
                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A91653; MUID:72189444
A;Accession: A91653
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F;57-88/Region: framework 3
F;57-88/Region: framework 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-107 <SHL>
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C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107
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DB 2;

12;

Indels Length 107;

Gaps

1972

Immunglobulin-L-Kette vom kappa-Typ,

methods

P.,

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RESULT 15

Ig kappa chain (BRE) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C;Accession: I39154
R;Schormann, N; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A;Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed A;Reference number: I39154; MUID:96003804
A;Reference number: I39154; MUID:96003804
A;Accession: I39154
A;Ccession: RRAA
A;Residues: 1-108 <RES>
A;Cross references: EMBL:U31344; NID:9944925; PIDN:AAA79238.1; PID:g944926
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: S02572; MUID:88005152
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Gene: GDB:IGKV1
A;Gene: GDB:136264
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted
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Search completed: May
Job time: 198 sec
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Matches 85
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Best Local Similarity 79.4%;
Matches 85; Conservative
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                      2002, 12:23:47
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Pred. No. 2.1e-31;
8; Mismatches 13;
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Pred. No. 4.6e-31;
9; Mismatches 12;
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OM protein - protein search, using sw model
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Run on: May 7, 2002, 12:32:34; Search time 21.92 Seconds (without alignments) 177.303 Million cell updates/sec

Title:
Perfect score:
Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

US-09-155-739-7
562
1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table:

Searched: 100059 segs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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63.8	54.0	64.4	64.4	64.7	64.9	64.9	65.2		٠		67.9			68.4	68.6	68.8	69.1	69.5	70.6		71.6	72.7	72.8	72.9	73.6	74.6	74.6	74.6	75.0	78.2	78.9	Match	% Query
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60.3	60.3	60.4	60.6	60.7	60.8	61.4	61.5	61.6	61.9	62.0	63.4
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P01624 homo sapien	home	mus	mus	hom	mus.	mus	P01653 mus musculu	home	homo	homo	homo

ALIGNMENTS

LHUMAN STANDARD; PRT; 108 AA. PO1607; PO1607; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1986 (Rel. 01, Last sequence update) 16-Karyota Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi; 17-Representation of the tropetic peptides; the complete amino acid characterization of the tryptic peptides; the complete amino acid characterization of the tryptic peptides; the complete amino acid characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their hombiting site.", hybriol. Chem. 356:167-191(1975). 12] 12] 13. K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). 14. PROTEINE-7603968; PubMed-1182131; 15. PROPE-Seyler's Z. Physiol. Chem. 356:167-191(1975). 17. MEDILINE-7603968; PubMed-1182131; 17. PROPE-Seyler's Z. Schiffer M., Hubber R., Palm W.; 18. PROPE-Seyler's Z. Schiffer M., Hubber R., Palm W.; 19. ANAREX. 19. ANAREX. 19. ANAREX. 19. ANAREX. 19. ANAREX. 10. ANAREX.	THE PROPERTY OF THE PROPERTY O	KV10_H KV10_H ID K AC P DT 2 DT 2 DT 1 DE I OS H OC M
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.InterPro; IPRU035y..
. Pfam; PF00047; ig; 1.
.V SMART; SM00406; IGv; 1.
.VW Immunoglobulin V region; Bence-
.TN 24 34
.TN 35 49
.TN 35 49
.TN 35 49
.TN 36 88
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Best Local :
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                                                                                                                           Bence-Jones protein Au.";
Biophys. Struct. Mech. 1:139-146(1975).

-I- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V REGION OF THE KAPPA CHAIN REI.

-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

PIR; A01862; KIHOAU.

HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   P01594;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG KAPPA CHAIN V-I REGION AU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAND
                                                                                                                                                                                                                                                 MEDLINE-77022433; PubMed-1234024; Fehlhammer H., Schiffer M., Epp O., Schwager P., Steigemann W., Schramm
                                                                                                                                                                                                                                                                                                                        Schiechl H., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones protein Au).";
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY.
                                                                                                                                                                                                                                                                                                             Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=72189444; PubMed=5028201;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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81.1%;
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                                         Bence-Jones protein.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 443.5; DB 1
Pred. No. 5.7e-40;
                   FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING
          FRAMEWORK 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9E8143E1188BCE2A CRC64;
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                                                                                                                                                                                                                                                     H.J.;
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                                                                                       Query Match
Best Local
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DISULFID
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SEQUENCE
                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-199 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION LAY.
                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                              PIR; A01871; K1HULY. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                               Scand. J. Immunol. 5:677-684(1976).

-i- MISCLLANBOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDBNTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN, WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                specificities."
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete amino acid sequence of the variable domains of two IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capra J.D., Klapper D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=77038198; PubMed=824717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                    Local
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  61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
                          \vdash
                                      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                          DIQMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS
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79.4%;
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75.0%;
                                                                                                                                        11834 MW;
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                                                                           11;
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                                                                                      Score 421.5; DB 1
Pred. No. 1.2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 439.5; DB 1
Pred. No. 1.5e-39;
                                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING FRAMEWORK 2.
                                                                                                                                                                             COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING
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                                                                                                                                                                BY SIMILARITY.
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                                                                                                                                        739993A95431434A CRC64;
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                                                                                                  DB 1;
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RESULT 4

KVIA_HIMA 1

KVIA_HIMA 1

KVIA_HIMA 2

COLORDO S. 001593

DT 21-JUL

T 21-MI

CC -1- MI

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Best Local :
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Interpro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Ber
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG KAPPA CHAIN V-I REGION ROY.
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-I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A01861; K1HUAG. HSSP; P01607; 1REI.
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=69234734; PubMed=4893682;
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MEDLINE=68362076;
Hilschmann N.;
                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                  SEQUENCE
                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKKAPKILIYDASNLETGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                               PubMed=5595110;
                                                                                                                                                                 Chordata;
Primates;
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76.6%;
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Pred. No. 1.9e-37;
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COMPLEMENTARITY-DETERMINING
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                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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 RESULT 6
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                                                                                               MEDLINE-95086080; PubMed=7993911;
Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
Solomon A., Stevens F.J., Schiffer M.;
Solomon f crystal structures of two homologous proteins:
"Comparison of crystal structures of interactions in immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
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SEQUENCE
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Steinmetz-Kayne M., Suter L., V
(In) Franck F., Shugar D: (eds
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SMART; SM00406; IGv;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
[2]
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01-NOV-1995 (Rel.
15-JUL-1999 (Rel.
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                    Stevens F.J., Westholm F.A., Panagiotopoulos N., Popp R.A., Solomon A.;
                                                                                        structural origin of altered domain light-chain dimers.";
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Chemical structure of 2 kappa-type Bence Jones proteins (Roy
 related
                                            SEQUENCE OF 1-35.
MEDLINE=81267384;
                                                                             Biochemistry
                                                                                                                                                          SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                  Homo sapiens (Human)
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"Characterization and preliminary related fragment of the human kI E
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Pred. No. 1.9e-37;
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Best Local
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                                                                                                                                                                               kappa type (Bence-Jones protein Scw.), II: The chymotryptic and the complete amino acid sequence.";
Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1
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                                                                                                                                                                                                                                               MEDLINE=75059271;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                          Immunoglobulin
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                                                                              V region; Bence-Jones protein.
1 23 FRAMEWORK 1.
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COMPLEMENTARITY-DETERMINING 3.
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                                                                                                                                                               BENCE-JONES PROTEIN
       BY SIMILARITY.
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                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1
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                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Immunoglobulin genes of the Kappa light chain type from two human lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation updat
IG KAPPA CHAIN. V-I REGION WALKER PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                          DOMAIN
                                                                                                                                                      DOMAIN
                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KV1W_HUMAN
                                                                                                                                                                                                                                                                                         InterPro; IPR003006; Ig_MH
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                     [mmunoglobulin V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=85014148; PubMed=6091049;
                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGRDYTFTISSLOPEDIATYYCLOYDNL-WTFGOGTKVEIK 106
1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGTDFTLTISTLQPEDIGNYYCQQYDNVPITFGQGTRVENK
                                                                                                                                                                                                                                                                                                                                           X00965; CAA25477.1; ALT_TERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
                                      ; 08
                                                  Similarity
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                                                                                                   129 AA;
                                     Conservative
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72
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111
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                                                                                                                                                                                                                                                       region;
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129
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                                                                                                   14069 MW;
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                                                 72.9%;
                                                                                                                                                                                                                                                                                                      Ig_MHC.
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                                                                                                                                                                                                                                                      Signal.
                                     10;
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                                  Pred. No. 2.6e-36;
0; Mismatches 16;
                                                            Score 409.5;
                                                                                                                           FRAMEWORK 4.
BY SIMILARIT
                                                                                                                                                               COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 413.5; DB 1
Pred. No. 8.1e-37;
                                                                                                                                                   COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                        FRAMEWORK 2
                                                                                                                                                                                                                  FRAMEWORK
                                                                                                                                                                                                                              IG KAPPA CHAIN V-I REGION WALKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                   F941FA07D4AFC2F9 CRC64;
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                                                            DB 1;
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                                                            Length 129;
                                    Indels
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23 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVTS

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RESULT 9
KV1D_HUMAN
                    RVIRGHT RAVIRGE TO THE TOTAL TOT
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Best Local
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P01610;
21-JUL-1986
Goni F., Frangione B.;
Goni F., Frangione B.;
Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal I (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region;
CARBOHYD 28 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eur. J. Biochem. 49
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Milstein C.P., Deverson E.V.;
"Primary structure of kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG KAPPA CHAIN V-I REGION CAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P01596;
21-JUL-1986
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                                                                                                                                 MEDLINE=83273707; PubMed=6410398;
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
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                                                                                                                                                                                                                                                                                    KAPPA CHAIN V-I REGION WEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A01864; K1HUAR.
; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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IPR003596; Ig_v.
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107
107
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S: THE C REGION OF THIS CHAIN HAS
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N-LINKED
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Pred. No. 2.
                                                                                                                                                                                                                        Catarrhini; Hominidae;
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                                                                                                                                                                                                                                           Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                                                                                                                             Euteleostomi;
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KV1H_HUMAN
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Best Local
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003596; Pfam; PF00047; ig; 1. SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                    KV1H_HUMAN
P01600;
DISULFID NON_TER
                                                                                                                                                        Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(197-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS -:- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WALDENSTROM'S MACROGLOBULINEMIA. PIR; A01876; K1HUWE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WIT
                                                                                                                                                                                             chain of subgroup
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin
                                                                                              Pfam; PF00047; ig; 1
SMART; SM00406; IGV;
                                                                                                                                                                                      subgroups."
                                                                                                                                                                                                                             MEDLINE=71032830;
                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                   DOMAIN
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                                                                  DOMAIN
                                                                             DOMAIN
                                                                                      Immunoglobulin
                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                     HSSP; P80362;
                                                                                                                                               PIR; A01868; K1HUHU.
                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                               KAPPA CHAIN V-I REGION HAU
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77; Conserv
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structure of a monoclonal kappa-type immunoglobulin
group I (Bence-Jones Protein Hau): subdivision withir
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                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                      01, Created)
01, Last sequence update)
38, Last annotation update)
                                                                                                                                                                                                                           PubMed=4097974;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.7%;
72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody.
                                                                                      Bence-Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 408.5; DB 1
Pred. No. 2.7e-36;
2; Mismatches 17
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
BY SIMILARITY.
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                                      COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
                                                                            FRAMEWORK 1.
                   COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
                                                          FRAMEWORK
                                                                  COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9249B61F0945618C CRC64;
          SIMILARITY
                                                                                                                                                                 351:1291-1295(1970).
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                                                                                                                                                                                                                                                                  Hominidae;
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                                                                                                                                                                   VNI
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SEQUENCE

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                                                                                                                                                          Query Match
Best Local (
                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                   Immunoglobulin V region.

DOMAIN 24 34

DOMAIN 25 49

DOMAIN 50 56

DOMAIN 57 88

DOMAIN 89 97

DOMAIN 89 107

DOMAIN 98 107

DOMAIN 98 107

DOMAIN 98 107
                                                                                                                                                                                                                                                       DISULFID NON_TER
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003596; Pfam; PF00047; ig; 1 SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 9:3188-3196(1970).

-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."; Biochemistry 9:3155-3161(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created
21-JUL-1986 (Rel. 01, Last see
15-JUL-1999 (Rel. 38, Last an
IG KAPPA CHAIN V-I REGION EU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A01866; K1HUEU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gall W.E., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01607; 1REI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Intrachain disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The covalent structure of a human gamma G-immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=71064027; PubMed=4923144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=71064023; PubMed=5489770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KV1F_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
              61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYD-NLWTFGQGTKVEIK 106
                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                          ساور
                                                                           1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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                                                    DIQMTQSPSTLSASVGDRVTITCRASQSINTWLAWYQQKPGKAPKLLMYKASSLESGVPS
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Similarity
                                                                                                                                                                                                                                     108 AA;
                                                                                                                                      Conservative
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01, Last sequence update)
38, Last annotation update)
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                                                                                                                                                                                                                                   11788 MW;
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                                                                                                                                      16;
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                                                                                                                                                      Score 397.5; DB 1
Pred. No. 3.9e-35;
                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY-DETERMINING FRAMEWORK 3.
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Pred. No. 1.2e-35;
                                                                                                                                                                                                                                                                                            FRAMEWORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                   9CD294F2F4D88823 CRC64;
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                                                                                                                                    Mismatches
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DB 1;
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                                                                                                                                                                        Length 108;
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В
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RESULT 13
KV1V_HUMAN
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NON_TER
SEQUENCE
"Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker."; J. Blochem. 77:1277-1296(1975).

-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
IG KAPPA CHAIN V-I.
                                                                                                                                                                                                                                                                                          P01603;
                                                                         Shinoda T
                                                                                           MEDLINE=76189985; PubMed=818073;
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                 KV1K_HUMAN
                                                                                                                 SEQUENCE
                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                       Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dwulet F.E., O'Connor T.P., Benson M.D.;
"Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
MOI. Immunol. 23:73-78(1986).
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-I REGION BAN.
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InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                      61 NFTGSGSGTDFILTISSLQPEDFATYYCQQYNSYPYTFGQGTKVQIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
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75; Conserv
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.089
                                                                                                                                                                                                                                                                                                               STANDARD;
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107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 396.5; ; Pred. No. 5e-: 14; Mismatches
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                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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PIR; A01869; K1HUKA.

- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

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RESULT 15

KVIE_HUMAN

KVIE_HUMAN

CRUEL_HUMAN

AC

P01597;

DT

21-JUL-1986 (Rel. 01, Created)

DT

21-JUL-1986 (Rel. 01, Last sequence update)

DT

15-JUL-1999 (Rel. 38, Last annotation update)

DE

IG KAPPA CHAIN V-I REGION DEE.

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebra

OC

Mammalia; Eutheria; Primates; Catarrhini; Homini

OC

Mammalia; Eutheria; Primates; Catarrhini; Homini

OC

Mammalia; Pubmed-5124396;

RN

[1]

RP

SEQUENCE.

RN

MILSTein C.P., Deverson E.V.;

RT

"The amino acid sequence of a human kappa light of the sequence of a human light of the sequence of a h
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Best Local S
Matches 71
Query Match
Best Local Similarity
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DOMAIN 1
DOMAIN 24
DOMAIN 35
DOMAIN 50
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DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 tein C.P., Deverson E.V.;
amino acid sequence of a human kappa light chain.";
hem. J. 123:945-958(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
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69.1%;
68.9%;
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Pred. No. 2.1e-34;
9; Mismatches 16
Score
Pred.
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BY SIMILARITY.
                                                                                                                        FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 2.

COMPLEMENTARITY-DETERMINING
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                                                                                   BDD6E350017F1E51 CRC64;
388.5; DB 1;
No. 3.4e-34;
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                 Length 108;
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       RFSGSGSGRDYTFTISSLQPEDIATYYCLQ~YDNLWTFGQGTKVEI
                                                         73;
                                                         Conservative
                                                         13;
                                                         Mismatches
                                                         19;
                                                         Indels
106
             105
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Search completed: May Job time: 565 sec

7, 2002, 12:32:34

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                         SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   May 7, 2002, 12:31:42; Search time 67.26 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                      sp_phage:*
                                                                                                                                                                                                                                                                         sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                         sp_organelle:*
                                                                                                                                                                                                                                                      sp_mhc:*
                                                                                     sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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SUMMARIES

Result No.	Score	Query Match	Length	DB	Ħ	Description
_	428.5	76.2	108	4	Q9UL77	Q9u177 homo sapien
2	406.5	72.3	108	4	Q9UL70	Omo
ω	395	70.3	107	4	Q9UL81	homo
4	385.5	68.6	108	4	Q9UL79	
Çī,	384.5	68.4	214	11	Q9R1A5	Q9rla5 mus musculu
O	362.5	64.5	107	11	Q9JL84	mus
7	337.5	60.1	298	11	Q9QYF0	mus
8	336.5	59.9	108	4	Q9UL83	Q9u183 homo sapien
9	332	59.1	109	4	Q9UL85	
10	331	58.9	109	4	Q9UL78	Q9u178 homo sapien
11	329	58.5	109	4	Q9UL86	
12	307.5	54.7	107	11	Q9ERZ9	Q9erz9 mus musculu
13	302.5	53.8	99	11	Q9JL74	Q9j174 mus musculu
14	297	52.8	106	υī	Q9U410	Q9u410 schistosoma
15	294	52.3	238	11	Q99M37	Q99m37 mus musculu
16	292.5	52.0	114	4	Q9UL80	Q9u180 homo sapien
17	284.5	50.6	101	11	Q9JL78	Q9j178 mus musculu
18	281.5	50.1	97	11	Q9JL76	Q9j176 mus musculu
19	273.5	48.7	109	σ	Q9NOW5	Q9n0w5 oryctolagus

ALIGNMENTS

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RESULT
Q9UL77
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Best Local Similarity
Matches 82; Conserval
                                                                                                                                                                                             EMBL; AF035037; AAD56273.1; -.
HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfan; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
NON_TER
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Q9UL77;
                                                                                                                                                                              NON_TER
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MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             Young D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                 fetus."
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61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
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                                             DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                               DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS
                                                                                                                                                               108 AA; 11738 MW;
                                                                                                                                                                              108
                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                     76.2%; score 428.5; DB 4; 76.6%; Pred. No. 3.3e-40; tive 8; Mismatches 16;
                                                                                                                                                                C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 AA
                                                                                         Indels
                                                                                                                   Length 108;
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RESULT QUARTE COLOR RESULT CO
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Q9UL81; PRESIDENT CONTROL OF CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
EMBL; AF035033; AAD56269.1;
                                                                                                                                                                                                                                     Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Young D.C.;
                                                                                                                                                                                                                                                                                                               MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                         Clin, Immunol. Immunopathol. 87:18
                                                                                                                                                            retus.
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                                                                                                                                                                                        Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                             DOMAIN
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108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11633 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                  87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 406.5; DB 4
Pred. No. 9.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                              AND
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                                                                              MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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                                                                              HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                      Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 108;
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                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9UL79;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF035035; AAD56271.1; HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=98277139; Pubmed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003006; Ig
InterPro; IPR003596; Ig
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P80362; 1WTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coung D.C.
                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
                    U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN.
                                                                                             RFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK
                                                                                                                                       RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu B., Van der Merwe P.L., Kalis N.N.,
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             108
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
11501 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                             108
                                                                                                                                                                                                                                                                                                                                                                                                                      11787 MW;
                                                                                                                                                                                                                                                                                                                   68.6%;
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71.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I9_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;; Score 395; DB 4; 1; Pred. No. 1.7e-36; 10; Mismatches 20;
                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                   Score 385.5;
Pred. No. 2e
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                                                                                                                                                                                                                                                                                                                                                                                                                 DB5845F19724FB4E CRC64;
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                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                           21;
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                                                                                                                                                                                                                                                                                           Indels
                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                         Gaps
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Q9R1A5 Q9R1A5;

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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 71
   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.; "Cloning of cDNAs encoding for anti-white pine blister rust antibody (Mab 7, its light and heavy chains) and constructic single chain antibody (scFV)."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                               NON_TER
                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                      acetyl-glucosamine antibodies from mice with autoimmune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                  Malkiel S., Liao L., Cunningham M.W., Diamond B.; "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9JL84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9JL84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                            SMART;
                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P01789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                        interPro;
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                                                                                                                                                                                                                                                                           DOMAIN.
                                                                                                                                                                                                                                                                                                          SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00047; ig;
                                                                                                                                                                                                                                    AF206022; AAF69320.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF152371; AAD40242.1; -.
                                                                                                     SM00406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                              IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003600; Ig_like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
   107
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 AA;
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InterPro; IPR003596; IÇ
Pfam; PF00047; 19; 2.
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01-MAY-2000
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C; TISSUE-SPLEEN; Shinohara N., Demura T., Fuku Submitted (DEC-1999) to the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
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01-JUN-2001
    MYOSIN-REACTIVE
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EMBLrel. 13, Created)
EMBLrel. 13, Last sequence update)
EMBLrel. 17, Last annotation update)
IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
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31867
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Pred. No. 1.4e
19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E0F96B8A17004317 CRC64;
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01-MAY-2000 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
HOmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
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MEDLINE=98277139; PubMed=9614934;
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                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003596; Ig_v
                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fetus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fetus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNN-WPFTFGPGTKVDIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF035029; AAD56265.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol. Immunopathol. 87:184-192(1998)
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                                                                                                                                                        109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                    11761 MW;
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60.2%;
59.1%;
61.5%;
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Pred. No. 5.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.L.,
Score 332;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                        FB1E43E7C7AFACCC CRC64;
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2; DB 4;
. 1.8e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berney S.M.
                                Length 109;
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RESULT
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O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE
 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.
                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TIEMBLIE1 13, Created)
01-MAY-2000 (TIEMBLIE1 13, Last sequence update)
01-JUN-2001 (TIEMBLIE1 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                             NCBI_TaxID=9606;
                                                                                                                                                                                        Q9UL86
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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SMART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fetus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roung D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                           60 SRFSGSGSGRDYTFTISSLQPEDIATTYCLQY-DNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                           61 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108
                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                     1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                  1 DIQMTQSPSSLSASVGDRVTITCKTSQDI-NKYMAWYQQTPGKAPRLLIHYTSALQPGIP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                109
109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003006;
                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              der Merwe P.L., Kalis N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11646 MW;
                                                                                                                                                                                                                                                                                                                                                                                         58.9%;
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P.L.,
                                                                                                                                                                                                                                                                                                                                                                                       Score 331; DB 4;
Pred. No. 2.3e-29;
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                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Kalis N.N.,
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 Berney S.M.
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 109;
                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                  REGION (FRAGMENT).
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RESULT
Q9ERZ9
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Best Local Similarity
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Best Local
                                            Pfam; PF00047; 1g; 1
SMART; SM00409; IG; 1
SMART; SM00406; IGv; 1
NON_TER 107 107
SEQUENCE 107 AA; 11784
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;

"Cloning and sequencing of the light chain fragment of variable region genes of an anti-hTMF-a monoclonal antibody.";

" ^~11 Mol. Immunol. 12:21-26(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | HSSP; | PUL/U/
| InterPro; | IPR003006; | Ig_MHC.
| InterPro; | IPR003596; | Ig_v.
| Pfam; | PF00047; | Ig; | 1.
| SMART; | SM00406; | IGv; | 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                SEQUENCE FROM N.A.

Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B.,
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ dar
                                                                                                                                                                                                                              Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., "Construction and sequencing of the single-chain human TNF-alpha specific monoclonal antibody."; Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9ERZ9;
                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                               InterPro;
                                                                                                                          InterPro;
                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                       SIMILARITY: TO IMMUNOGLOBULIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRFSGSGSETDFTLTISRLEPEDFAVYYCQQYGSSIFTFGPGTKVDIK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRFSGSGGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
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                                                                                                                                              AF262753; AAG23804.1;
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                                                                                                        IPR003599; Ig.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                11784 MW;
  54.7%;
53.3%;
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Score 307.5; DB 1
Pred. No. 9.3e-27;
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Pred. No. 3.
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                                              2B15EEA6604A26C3 CRC64;
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           DB 11;
                                                                                                                                                                   3J databases.
HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                                                                                                                      Su C.Z.; antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 109
                                                                                                                                                                                           Su C.Z.;
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          Length 107;
                                                                                                                                                                                                                                                                                                                                                                                         Murinae; Mus
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Q9JL74
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                                                                                                          01-MAY-2000 (TrEMBLrel 13, Last sequenc 01-JUN-2001 (TrEMBLrel 17, Last annotat MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 VARIABLE REGION (FRAGMENT).
  Song X.T., Feng "Amplification,
                           SEQUENCE FROM N.A.
                                                                                                Schistosoma japonicum (Blood fluke).
                                                                                                                                                                Q9U410;
01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                           Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Trematoda; Digenea; Strigeidida; Schistosomatoidea;
                                                                                                                                                                                            090410
                                                  NCBI_TaxID=6182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malkiel S., Liao L., Cunningham M.W., Diamond B.;

"Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TremBLrel. 15, Created)
01-OCT-2000 (TremBLrel. 15, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF206032; AAF69330.1;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/C;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                            71 YTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
                                                                                                                                                                                                                                                                                                                  11 LSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPSRFSGSGSGRD
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                                                                                                                                                                                                                                                     FTFTISTVQAEDLAVYFCQQDYSSPRTFGGGTKLEIK 99
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cloning
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58.8%;
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 and sequ
                                                                                                                                    13, Created)
13, Last sequence update)
17, Last annotation updat
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.N., Li Y.Q., sequence anal
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                                                                                                                                                                                                                                                                                                                                                                     Score 302.5;
Pred. No. 3.
                                                                                                                                                                                         PRT;
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analysis
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hes 23;
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Huang H.L.,
lysis of the
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                                                                         Neodermata;
Schistosomatidae;
Guan X.H.;
light chain
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RESULT 15
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Search completed: May Job time: 628 sec
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                                                                                                                                                                              Query Match 52.3%; Score 294; DB 11; Length 238; Best Local Similarity 50.0%; Pred. No. 7.4e-25; Matches 56; Conservative 22; Mismatches 28; Indels
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP0047; 19; 1.
SMART; SM00406; IGv; 1.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                  099M37;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:5947).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                           TISSUE=MAMMARY TUMOR;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99м37
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                                                                                                                         63 GSGSGTSYSLTISRMEAEDAATYYCQQWTSYPFTFGSGTKLELK 106
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                                                                    106 AA;
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              7,
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             2002, 12:31:42
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